

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 13:28:23 ; Search time 1496.84 Seconds

(Without alignments)
10479.665 Million cell updates/sec

Title: US-09-852-261-3

Perfect score: 539

Sequence: 1 ggaacagagacaccttcgag.....agtaaacattcccggaattc 539

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	539	100.0	539	AX147744	AX147744 Sequence
2	539	100.0	539	AX300781	AX300781 Sequence
3	539	99.4	710	RATIGFIA	M15680 Rat Insulin
4	516.6	95.8	798	RNIGF12	X06108 Rat mRNA (c
5	516.6	95.8	958	RNIGF12	X06107 Rat mRNA (c
6	470.2	87.2	1536	BC012409	BC012409 Mus muscu
7	453.8	84.2	651	MMIGFIBR	X04482 Mouse mRNA
8	425	78.8	487	AX147752	AX147752 Sequence
9	425	78.8	487	AX300789	AX300789 Sequence
10	421.8	78.3	1346	RATIGFIB	M15681 Rat Insulin
11	402.6	74.7	1052	RATIGFIA	D00698 Rattus sp.
12	401	74.4	513	RATGJIL	M17714 Rat Insulin
13	387	71.8	826	RATIGFIA	X06043 Rat mRNA fo
14	387	71.8	826	RATIGFIA	M17335 Rat Insulin
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16	356.8	66.2	523	AX147746	AX147746 Sequence
17	356.8	66.2	523	AX300783	AX300783 Sequence
18	325.2	60.3	517	AX147742	AX147742 Sequence
19	325.2	60.3	517	AX300779	AX300779 Sequence
20	274.2	50.9	7260	AX375028	AX375028 Sequence
21	274.2	50.9	7260	AX411095	AX411095 Sequence
22	274.2	50.9	7260	HSIGFACI	X57025 Human IGF-I
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24	272.6	50.6	725	HSIGFI	X00173 Homo sapien
25	272.6	50.6	728	HUMGFII	M29644 Human Insul
26	271.2	50.3	616	HSIGFIA	X56773 H.sapiens m
27	271.2	50.3	620	HSIGFIA	X08370 Sequence 2
28	270	50.1	1076	HUMIGFI	M27544 Human Insul
29	268.8	49.9	444	HSU40870	A04870 Human alter
30	267.2	49.6	432	AF022961	AF022961 Oryctolag
31	262	48.6	471	AX147754	AX147754 Sequence
32	262	48.6	471	AX300791	AX300791 Sequence
33	260	48.2	567	PIGGRFIA	M31175 Pig Insulin
34	258	47.9	532	SEIIGFIM	X17492 Porcine mRN
35	237.4	44.0	888	ECU85272	U85272 Equus cabal
36	231	42.9	730	HSIGFIB	X56774 H.sapiens m
37	231	42.9	1094	HUMGFIB	M11568 Human Insul
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39	231	42.9	1136	I08009	I08009 Sequence 3
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44	228.6	42.4	1284	BTIGFIA	X15726 Bovine mRNA
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ALIGNMENTS

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RESULT 1
AX147744
LOCUS AX147744 539 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 3 from Patent WO0136483.
ACCESSION AX147744
VERSION AX147744.1 GI:14346789
KEYWORDS
SOURCE
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 539)
AUTHORS Goldspink, G.R. and Johnson, I.R.
TITLE Use of the insulin-like-growth factor 1 isoform mgf for the
```

JOURNAL
treatment of neurological disorders
Patent: WO 0136483-A 3 25-MAY-2001;
University College London (GB)

FEATURES

source
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Location/Qualifiers
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CDS

BASE COUNT
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ORIGIN

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Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 CTGCTTGAGCAACCTTCGAAACATGGAGACACCTGCAATTCATATATGATGATGATG 480
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RESULT 2

AX300781 539 bp DNA linear PAT 30-NOV-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0185781.
ACCESSION AX300781
VERSION AX300781.1 GI:17382062
KEYWORDS
SOURCE
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 Goldslink, G.D. and Terenghi, G.B.

TITLE
Repair of nerve damage
Patent: WO 0185781-A 3 15-NOV-2001;
University College London (GB); East Grinstead Medical Research
Trust (GB)

FEATURES

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CDS

BASE COUNT
161 a 136 c 139 g 103 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 539; DB 6; Length 539;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGACAGAGACCCCTTTCGGGGCTGAGCTGTGAGAGCTCTTCACTTGTGTGACCA 60
QY 61 AGGGGCTTTTACTTCAACAAGCCACAGCTATGGCTCCAGCATTCGAGGGCACCCACAG 120
DB 61 AGGGGCTTTTACTTCAACAAGCCACAGCTATGGCTCCAGCATTCGAGGGCACCCACAG 120
QY 121 ACGGGCTTTTGTGATGATGTTGCTTCGAGCTGTGAGAGGCTGAGATGTAC 180
DB 121 ACGGGCTTTTGTGATGATGTTGCTTCGAGCTGTGAGAGGCTGAGATGTAC 180
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DB 181 TGTGTCGGCTGCAAGCTCAAAAGTCAGCTGCTCCAGAGCTGTGATGAGAGGCTGAGATGTAC 240
QY 241 ATGCCCAAGACTAGAGAGTCCAGCCCTATGACACACAAAGAAAGAAAGCTGCAAGG 300
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DB 421 CTGCTTGAGCAACCTTCGAAACATGGAGACACCTGCAATTCATATATGATGATGATG 480
QY 481 TCATTTTCAGAGATGGGCAATTCCTTCATGAATACACAAAGTAACATTCGCGAATTC 539
DB 481 TCATTTTCAGAGATGGGCAATTCCTTCATGAATACACAAAGTAACATTCGCGAATTC 539

RESULT 3

RAT1GFIA 710 bp mRNA linear ROD 27-APR-1993
LOCUS
DEFINITION Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION M15480
VERSION M15480.1 GI:204749
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 710)

AUTHORS Roberts, C.T. Jr., Lasky, S.R., Lowe, W.L. Jr., Seaman, W.T. and Lebois, D.

TITLE Molecular cloning of rat insulin-like growth factor I complementary deoxyribonucleic acids: differential messenger ribonucleic acid processing and regulation by growth hormone in extrahepatic tissues

JOURNAL Mol. Endocrinol. 1 (3), 243-248 (1987)

MEDLINE 88288198

PUBMED 3453891

COMMENT Draft entry and computer-readable copy of sequence in [Mol. Endocrinol. (1987) in press] kindly provided by S.R. Lasky, 16-Mar-1987.

FEATURES

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BASE COUNT 202 a 191 c 172 g 145 t

ORIGIN 1 bp upstream of EcoRI site.

Query Match 99.4%; Score 535.8; DB 10; Length 710;
Best Local Similarity 99.6%; Pred. No. 9.9e-158;
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 232 AGGGCTTTTACTTCAACAAGCCCAAGTATGAGCTCCAGATTGAGGAGGACACAG 291
QY 121 ACGGCAATTTGATGAGTGTGCTTCGGAGCTGTGATGTGAGAGGCTGGAGATGAC 180
DB 292 ACGGCAATTTGATGAGTGTGCTTCGGAGCTGTGATGTGAGAGGCTGGAGATGAC 351
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DB 532 CAGATATGAGAGAGAGCTCCCGAGGAAAGAAAGCCAGCTACCCGAAAGTCTTTG 591
QY 421 CTGCTTGAAGCAACCTGCAAAACATCGAAGACCTGCAAAATATCAATATGAGTTCA 480
DB 592 CTGCTTGAAGCAACCTGCAAAACATCGAAGACCTGCAAAATATCAATATGAGTTCA 651

QY 481 TCATTAGAGATGGGCAATTCCTCTCAATGAATACACAGTAACATTCCTCCGGAATTC 539
DB 652 CCATTGAGAGATGGGCAATTCCTCTCAATGAATACACAGTAACATTCCTCCGGAATTC 710

RESULT 4

LOCUS R18GFI2

DEFINITION Rat mRNA (clone IGF1a2) for insulin-like growth factor I.

ACCESSION X06108 M2339 J00429

VERSION X06108.1 GI:56426

KEYWORDS insulin-like growth factor I.

SOURCE Rattus norvegicus.

ORGANISM Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 798)
AUTHORS Rotwein, P.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1987) Rotwein P., Washington University, School of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO 63110, USA

REFERENCE 2 (bases 1 to 798)
AUTHORS Shimatsu, A. and Rotwein, P.
TITLE Sequence of two rat insulin-like growth factor I mRNAs differing within the 5' untranslated region
JOURNAL Nucleic Acids Res. 15 (1987) in press
COMMENT Another IGF-I mRNA of rat liver differing in the 5' UT-region is described in <X06107>.

FEATURES

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Matches 522; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTCGGGGCTGAGCTGTGAGCCCTTCAGTCTGTGTGACCA 60
DB 217 GGACCAAGACCCCTTCGGGGCTGAGCTGTGAGCCCTTCAGTCTGTGTGACCA 276
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DB 277 AGGGCTTTTACTTCAACAAGCCCAAGTATGAGCTCCAGATTGAGGAGGACACAG 336
QY 121 ACGGCAATTTGATGAGTGTGCTTCGGAGCTGTGATGTGAGAGGCTGGAGATGAC 180
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QY      361 CAGAAATGAGAGAGAGCTCCCGAGAACAGAAATGCGACAGTCCGACCAAGATCTTTG 420
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Db      637 CTGCTTGAGCAACCTGCAAAACATGGAACACCTCCCAATATCATATATAGTTCATA 696
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RESULT 5
LOCUS   RNIF11 958 bp mRNA linear ROD 12-SEP-1993
DEFINITION Rat mRNA (clone IGFIAB1) for insulin-like growth factor I.
ACCESSION X06107 M32260 Y00429
VERSION X06107.1 GI:56424
KEYWORDS insulin-like growth factor I.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.

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REFERENCE
AUTHORS Rotwein, P.
TITLE Direct Submission.
JOURNAL Submitted (21-OCT-1987) Rotwein P., Washington University, School
of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
63110, USA

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REFERENCE
AUTHORS Shimatsu, A. and Rotwein, P.
TITLE Sequence of two rat insulin-like growth factor I mRNAs differing
within the 5' untranslated region.
JOURNAL Nucleic Acids Res. 15 (17), 7196 (1987)
MEDLINE 88015572
PUBMED 3658684

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COMMENT Another IGF-I mRNA of rat liver differing in the 5' UT-region is
described in <X06108>.

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FEATURES
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Location/Qualifiers

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BASE COUNT 260 a 246 c 209 g 243 t
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Query Match 95.8%; Score 516.6; DB 10; Length 958;
Best Local Similarity 98.3%; Pired. No. 1.2e-151;
Matches 522; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db      583 TGTGTCCGCTGCAAGCTTCAAAAGTCAAGTCTGTTCCATCCGGGCCACGCTACCTGAC 642
QY      241 ATGCCCAAGACTCAGAGTCCAGCCCTATGACACACAGAAAGAAAGAGACCTCAAGG 300
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QY      361 CAGAAATGAGAGAGAGCTCCCGAGAACAGAAATGCGACAGTCCGACAGATCTTTG 420
Db      763 CAGAAATGAGAGAGAGCTCCCGAGAACAGAAATGCGACAGTCCGACAGATCTTTG 822
QY      421 CTGCTTGAGCAACCTGCAAAACATGGAACACCTCCCAATATCATATATAGTTCATA 480
Db      823 CTGCTTGAGCAACCTGCAAAACATGGAACACCTCCCAATATCATATATAGTTCATA 882
QY      481 TCATTTCAGAGATGGGCAATTCCTCATGAATACAGACAGTAACATTC 531
Db      883 CCATTTCAGAGATGGGCAATTCCTCATGAATACAGACAGTAACATTC 933

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RESULT 6
LOCUS   BC012409 1536 bp mRNA linear ROD 07-AUG-2002
DEFINITION Mus musculus, Similar to Insulin-like growth factor I, clone
MGC:18617 IMAGE:4194295, mRNA, complete cds.
ACCESSION BC012409
VERSION BC012409.1 GI:15214568
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission.
JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

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REMARK
COMMENT Contact: MGC help desk
Email: gcabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center: Baylor College of Medicine Human Genome
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
Yoon, V.S., Kovis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 24 Row: K Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754307.
Location/Qualifiers

FEATURES

Source

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/organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
/clone="MGC:18617 IMAGE:4194295"
/tissue_type="Liver, normal, 5 month old male mouse."
/clone_lib="NCI CGAP_L19"
/lab_host="DH10B"
/note="Vector: PCMV-SPORE6"
28..429
/codon_start=1
/product="Similar to insulin-like growth factor 1"
/protein_id="AAH12409.1"
/db_xref="gi:15214569"
/translation="MSSSHLYLALCLITFTSSTTAGPETICGAELVDAIOFVCGPRG
FTFNKPTGSSIRAPOTGIYDECFSCDLRLMLCAPLKPTKARSIRORHTD
MERTQSPSLSTNKKTKLQRRKSGSTFEHR"

CDS

BASE COUNT 485 a 324 c 303 g 424 t
ORIGIN

Query Match 87.2% Score 470.2; DB 10; Length 1536;
Best Local Similarity 92.8%; Pred. No. 5.9e-137;
Matches 493; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GGACCGAGAGACCCCTTGGCGGGCTGAGCTGGTGGACGCTCTTCACTTGTGTGGACCA 60
DB 94 GGACCGAGAGACCCCTTGGCGGGCTGAGCTGGTGGACGCTCTTCACTTGTGTGGACCG 153
QY 61 AGGGGCTTTACTTCAACAGCCCAAGCTCTGTGCTCCAGATTCGAGGCGACCAAC 120
DB 154 AGGGGCTTTACTTCAACAGCCCAAGCTCTGTGCTCCAGATTCGAGGCGACCAAC 213
QY 121 ACGGCGATTGTGATGAGTGTGCTTCGAGAGCTGTATCTGAGAGGCTGGAGATGTAC 180
DB 214 ACGGCGATTGTGATGAGTGTGCTTCGAGAGCTGTATCTGAGAGGCTGGAGATGTAC 273
QY 181 TGTGTCCGCTGCAAGCTCAAGAGTCAAGTGTCTTCATCCGAGGCGACGACACAGTAC 240
DB 274 TGTGTCCGCTGCAAGCTCAAGAGTCAAGTGTCTTCATCCGAGGCGACGACACAGTAC 333
QY 241 ATGCCCAAGCTCAGAGTCCAGCCCTATTCAGACACAAAGAAAGAGAGCTGCAAGG 300
DB 334 ATGCCCAAGCTCAGAGTCCAGCCCTATTCAGACACAAAGAAAGAGAGCTGCAAGG 393
QY 301 AGAAGGAAGAGAGTCACTTGAAGACAAAGTAGAGAGAGTGCAGAGAAACAGACCTA 360
DB 394 AGAAGGAAGAGAGTCACTTGAAGACAAAGTAGAGAGAGTGCAGAGAAACAGACCTA 453
QY 361 CAGATGTGAGAGAGAGCTCCGAGAGACAGAAATGCCACGTCACCGCAAGATCCTTG 420
DB 454 CAGATGTGAGAGAGAGCTCCGAGAGAGACAGAAATGCCACGTCACCGCAAGATCCTTG 513
QY 421 CTGCTTGAGCAACCTCAGAAACATGGAACACCTCCAAATATCATATGATGATGATA 480
DB 514 CTGCTTGAGCAACCTCAGAAACATGGAACACCTCCAAATATCATATGATGATGATA 573
QY 481 TCATTTCAAGATGGGATTTCCCTCATGAATACAGAGTAACATTC 531
DB 574 ACATTCAGAAAGATGGGATTTCCCTCATGAATACAGAGTAACATTC 624

RESULT 7

MMIGTIBR

LOCUS MMIGTIBR 651 bp mRNA linear ROD 21-MAR-1995
DEFINITION Mouse mRNA for preproinsulin-like growth factor IB.
ACCESSION X04482
VERSION X04482.1 GI:51806
KEYWORDS growth factor; insulin-like growth factor IB; preproinsulin-like growth factor IB; signal peptide.

SOURCE

Mus musculus
ORGANISM

REFERENCE

1 (bases 1 to 651)
AUTHORS

Bell, G.I., Stemple, M.M., Fong, N.M. and Rall, L.B.
TITLE

Sequences of liver cDNAs encoding two different mouse insulin-like
growth factor I precursors
JOURNAL

Nucleic Acids Res. 14 (20), 7873-7882 (1986)
MEDLINE

87040760
PUBMED

3774549
COMMENT

The sequence is identical to the preproIGF-1A sequence (X04480) except for the presence of a 52 bp insertion following codon 86 (position 397 to 448), caused by alternative RNA splicing. The B domain of IGF comprises residues 1-29 (position 139-225), the C domain residues 30-41 (position 226-261), the A domain residues 42-62 (position 262-324) and the D domain residues 63-70 (position 325-348). Location/Qualifiers

FEATURES

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/strain="Bald/c"
/db_xref="taxon:10090"
/clone="m1gf1-4"
/tissue_type="Liver"
43..45
/note="pot. translation start"
73..474
/note="prepro IGF-1B (aa -22 to 111)"
/codon_start=1
/protein_id="CAA28170.1"
/db_xref="gi:51807"
/db_xref="MGI:96432"
/translation="MSSSHLYLALCLITFTSSTTAGPETICGAELVDAIOFVCGPRG
FTFNKPTGSSIRAPOTGIYDECFSCDLRLMLCAPLKPTKARSIRORHTD
MERTQSPSLSTNKKTKLQRRKSGSTFEHR"
73..138
sig_peptide
139..348
misc_feature
349..471
/note="mature IGF-1B (aa 1-70)"
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/note="COOH-terminal peptide (E domain) (aa 71 to 111)"
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misc_feature

43..45

CDS

BASE COUNT 193 a 185 c 149 g 124 t
ORIGIN
Query Match 84.2% Score 453.8; DB 10; Length 651;
Best Local Similarity 92.8%; Pred. No. 7.5e-137;
Matches 476; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 GGACCGAGAGACCCCTTGGCGGGCTGAGCTGGTGGACGCTCTTCACTTGTGTGGACCA 60
DB 139 GGACCGAGAGACCCCTTGGCGGGCTGAGCTGGTGGACGCTCTTCACTTGTGTGGACCG 198
QY 61 AGGGGCTTTACTTCAACAGCCCAAGCTCTGTGCTCCAGATTCGAGGCGACCAAC 120
DB 199 AGGGGCTTTACTTCAACAGCCCAAGCTCTGTGCTCCAGATTCGAGGCGACCAAC 258
QY 121 ACGGCGATTGTGATGAGTGTGCTTCGAGAGCTGTATCTGAGAGGCTGGAGATGTAC 180
DB 259 ACGGCGATTGTGATGAGTGTGCTTCGAGAGCTGTATCTGAGAGGCTGGAGATGTAC 318
QY 181 TGTGTCCGCTGCAAGCTCAAGAGTCAAGTGTCTTCATCCGAGGCGACGACACAGTAC 240
DB 319 TGTGTCCGCTGCAAGCTCAAGAGTCAAGTGTCTTCATCCGAGGCGACGACACAGTAC 378
QY 241 ATGCCCAAGCTCAGAGTCCAGCCCTATTCAGACACAAAGAAAGAGAGCTGCAAGG 300
DB 379 ATGCCCAAGCTCAGAGTCCAGCCCTATTCAGACACAAAGAAAGAGAGCTGCAAGG 438
QY 301 AGAAGGAAGAGTCACTTGAAGACAAAGTAGAGAGAGTGCAGAGAAACAGACCTA 360

439 AGAAGGAAGAGTACATTGGAAGAACACAGTAGAGAGTGCAGAAACAGACCTA 498
 361 CAGATATGAGAGAGAGCTCCCGAGAGACAGAAATGCCGCTACCCGCAAGTCTTTG 420
 499 CAGATATGAGAGAGAGCTCCCGAGAGACAGAAATGCCGCTACCCGCAAGTCTTTG 558
 421 CTGCTTGAAGCACTGCAAAACATCGAGACCTGCCAAATATCAATTAATGATTCATA 480
 559 CTGCTTGAAGCACTGCAAAACATCGAGACCTGCCAAATATCAATTAATGATTCATA 618
 481 TCATTTCAGAGATGGGCAATTCCTCATGATAA 513
 619 ACATTACAAAGATGGGCAATTCCTCATGATAA 651

RESULT 8
 AX147752 487 bp DNA linear PAT 08-JUN-2001
 LOCUS AX147752
 DEFINITION Sequence 11 from patent WO0136483.
 ACCESSION AX147752
 VERSION AX147752.1 GI:14346797
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 487)
 Goldspink, G. R. and Johnson, J. R.
 Use of the insulin-like growth factor I isoform mgf for the
 treatment of neurological disorders
 Patent: WO 0136483-A 11 25-MAY-2001;
 University College London (GB)
 Location/Qualifiers
 source 1..487
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
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 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC41179.1"
 /db_xref="GI:14346798"
 /translation="GPETLGGALVDALQFVGSGRGFEYFNKPTVYGSIRAPQGIY
 DECCFRSCDLRLLEMYCVRCCKPTKSARSIRAOHRHDMPTKQEVHLKNTSRSGAKNT
 YRM"

BASE COUNT 139 a 123 c 126 g 99 t
 ORIGIN
 Query Match 78.8%; Score 425; DB 6; Length 487;
 Best Local Similarity 90.4%; Pred. No. 8.8e-123;
 Matches 487; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

1 GGACCAAGAGACCTTTCCGGGGCTGAGCTGTGAGAGCTTTAGTCTGTGTGACCA 60
 1 GGACCAAGAGACCTTTCCGGGGCTGAGCTGTGAGAGCTTTAGTCTGTGTGACCA 60
 61 AGGGGCTTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGAGAGGACACACAG 120
 61 AGGGGCTTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGAGAGGACACACAG 120
 61 AGGGGCTTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGAGAGGACACACAG 120
 121 ACGGGCATTTGGATGAGTGTGCTTCCGAGAGCTGTGATCTGAGAGGCTGGAGATGAC 180
 121 ACGGGCATTTGGATGAGTGTGCTTCCGAGAGCTGTGATCTGAGAGGCTGGAGATGAC 180
 121 ACGGGCATTTGGATGAGTGTGCTTCCGAGAGCTGTGATCTGAGAGGCTGGAGATGAC 180
 181 TGTGTCCGCTGCAAGCTTACAAAGTCACTGCTTCATCCGAGCCACGACACTGAC 240
 181 TGTGTCCGCTGCAAGCTTACAAAGTCACTGCTTCATCCGAGCCACGACACTGAC 240
 241 ATGCCCAAGACTCAAGAGTCCAGCCCTATCGACACACAGAAAGAAAGTCTGCAAAAG 300
 241 ATGCCCAAGACTCAAGAGTCCAGCCCTATCGACACACAGAAAGAAAGTCTGCAAAAG 300
 301 AGAAGGAAGAGTACATTGGAAGAACACAGTAGAGAGTGCAGAAACAGACCTA 360

256 -----AAGGANTACACTTGAAGAACACAAATAGAGAGAGTGCAGAAACAGACCTA 308
 361 CAGATATGAGAGAGAGCTCCCGAGAGACAGAAATGCCGCTACCCGCAAGTCTTTG 420
 309 CAGATATGAGAGAGAGCTCCCGAGAGACAGAAATGCCGCTACCCGCAAGTCTTTG 368
 421 CTGCTTGAAGCACTGCAAAACATCGAGACCTGCCAAATATCAATTAATGATTCATA 480
 369 CTGCTTGAAGCACTGCAAAACATCGAGACCTGCCAAATATCAATTAATGATTCATA 428
 481 TCATTTCAGAGATGGGCAATTCCTCATGATAAATACAAAGTAAACATTCGCCGATTC 539
 429 TCATTTCAGAGATGGGCAATTCCTCATGATAAATACAAAGTAAACATTCGCCGATTC 487

RESULT 9
 AX300789 487 bp DNA linear PAT 30-NOV-2001
 LOCUS AX300789
 DEFINITION Sequence 11 from patent WO0185781.
 ACCESSION AX300789
 VERSION AX300789.1 GI:17382070
 KEYWORDS
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 487)
 Goldspink, G. D. and Terenghi, G. B.
 Repair of nerve damage
 Patent: WO 0185781-A 11 15-NOV-2001;
 University College London (GB) ; East Grinstead Medical Research
 Trust (GB)
 Location/Qualifiers
 source 1..487
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 /db_xref="taxon:10118"
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 /note="unnamed protein product"
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 /db_xref="GI:17382071"
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 DECCFRSCDLRLLEMYCVRCCKPTKSARSIRAOHRHDMPTKQEVHLKNTSRSGAKNT
 YRM"

BASE COUNT 139 a 123 c 126 g 99 t
 ORIGIN
 Query Match 78.8%; Score 425; DB 6; Length 487;
 Best Local Similarity 90.4%; Pred. No. 8.8e-123;
 Matches 487; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

1 GGACCAAGAGACCTTTCCGGGGCTGAGCTGTGAGAGCTTTAGTCTGTGTGACCA 60
 1 GGACCAAGAGACCTTTCCGGGGCTGAGCTGTGAGAGCTTTAGTCTGTGTGACCA 60
 61 AGGGGCTTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGAGAGGACACACAG 120
 61 AGGGGCTTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGAGAGGACACACAG 120
 61 AGGGGCTTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGAGAGGACACACAG 120
 121 ACGGGCATTTGGATGAGTGTGCTTCCGAGAGCTGTGATCTGAGAGGCTGGAGATGAC 180
 121 ACGGGCATTTGGATGAGTGTGCTTCCGAGAGCTGTGATCTGAGAGGCTGGAGATGAC 180
 121 ACGGGCATTTGGATGAGTGTGCTTCCGAGAGCTGTGATCTGAGAGGCTGGAGATGAC 180
 181 TGTGTCCGCTGCAAGCTTACAAAGTCACTGCTTCATCCGAGCCACGACACTGAC 240
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 241 ATGCCCAAGACTCAAGAGTCCAGCCCTATCGACACACAGAAAGAAAGTCTGCAAAAG 300
 241 ATGCCCAAGACTCAAGAGTCCAGCCCTATCGACACACAGAAAGAAAGTCTGCAAAAG 300
 241 ATGCCCAAGACTCAAGAGTCCAGCCCTATCGACACACAGAAAGAAAGTCTGCAAAAG 300

QY 301 AGAAGAAAGAGTACCTTGAAGACACACAGTAGAGAGTGCAGAAACAGACCTA 360
 Db 256 -----AAGGAGTACACTTGAAGAACACAACTAGAGAGTGCAGAAACAGACCTA 308
 QY 361 CAGAAATGTAGAGAGGCTCTCCAGAGAACAGAAATGCGACGTACCGCAAGATCTTTG 420
 Db 309 CAGAAATGTAGAGAGGCTCTCCAGAGAACAGAAATGCGACGTACCGCAAGATCTTTG 368
 QY 421 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCGCAATATCATATATGATTCAATA 480
 Db 369 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCGCAATATCATATATGATTCAATA 428
 QY 481 TCATTTCAGAGATGGGCACTTCCCTCAATGAATACAGATTAACATTCGGGAATTC 539
 Db 429 TCATTTCAGAGATGGGCACTTCCCTCAATGAATACAGATTAACATTCGGGAATTC 487

RESULT 10
 LOCUS RATIGFIB 1346 bp mRNA linear ROD 27-APR-1993
 DEFINITION Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
 ACCESSION M15481
 VERSION M15481.1 GI:204753
 KEYWORDS growth factor; insulin-like growth factor.
 SOURCE Rat (Sprague-Dawley) adult liver, cDNA to mRNA, clone pRIGF-1-25.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 1346)
 AUTHORS Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and Lerch,D.
 TITLE Molecular cloning of rat insulin-like growth factor I complementary deoxyribonucleic acids: differential messenger ribonucleic acid processing and regulation by growth hormone in extrahepatic tissues
 JOURNAL Mol. Endocrinol. 1 (3), 243-248 (1987)
 MEDLINE 88288198
 PUBMED 3453891
 COMMENT Draft entry and computer-readable copy of sequence in [Mol. Endocrinol. (1987) in press] kindly provided by S.R.Lasky, 16-MAR-1987.

FEATURES
 source location/Qualifiers
 CDS
 1..1346
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 794..1177
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 /translation="MSSSHLFLALCLITSSATAGPETICGAELVDALQFVGGPRG
 FYENKPTGSSIRAPQGTIVDECCFSCDLRLNEMCVCKRTKSRSTIRARHHD
 MPKTKVEVHLKMTSGSGNNTYRA"
 794..859
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 mat_peptide 1046..1069
 /product="Insulin-like growth factor D peptide"
 mat_peptide 1070..1174
 /product="Insulin-like growth factor E peptide"
 BASE COUNT 348 a 344 c 344 g 310 t
 ORIGIN 1 bp upstream of EcoRI site.

Query Match 78.3%; Score 421.8; DB 10; Length 1346;
 Best Local Similarity 90.0%; Pred. No. 1..1e-121;
 Matches 485; Conservative 0; Mismatches 2; Indels 52; Gaps 1;

QY 1 GGACGAGAGACCTTGGGGGCTGAGCTGTGAGACGCTTTCAGTTCGTGTGACCA 60

Db 860 GGACGAGAGACCTTGGGGGCTGAGCTGTGAGACGCTTTCAGTTCGTGTGACCA 919
 QY 61 AAGGCTTTTACTTCAACAGCCACACTGTATATGCTCAGATTCGGAGGCGACAG 120
 Db 920 AAGGCTTTTACTTCAACAGCCACAGCTATATGCTCAGATTCGGAGGCGACAG 979
 QY 121 ACGGCTTTTGTGATGAGTGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
 Db 980 ACGGCTTTTGTGATGAGTGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 1039
 QY 181 TGTGTCCCTGCAACCTTCAAAAGTCACAGTTCGTTCCATCCGGGCGCCACGCGAC 240
 Db 1040 TGTGTCCCTGCAACCTTCAAAAGTCACAGTTCGTTCCATCCGGGCGCCACGCGAC 1099
 QY 241 ATGCCCAAGACTCAGAGTCCCGGCCCTATGACACACAGAAAGGAAAGCTCAAAAG 300
 Db 1100 ATGCCCAAGACTCAG----- 1114
 QY 301 AGAAGAAAGAGTACACTTGAAAGACACAGTATAGAGAGTGCAGAAACAGACCTA 360
 Db 1115 -----AAGGAGTACACTTGAAGAACACAGTATAGAGAGTGCAGAAACAGACCTA 1167
 QY 361 CAGAAATGTAGAGAGGCTCTCCAGAGAACAGAAATGCGACGTACCGCAAGATCTTTG 420
 Db 1168 CAGAAATGTAGAGAGGCTCTCCAGAGAACAGAAATGCGACGTACCGCAAGATCTTTG 1227
 QY 421 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCCAATATCATATGAGTTCATA 480
 Db 1228 CTGCTTGAAGACCTGCAAAACATCGAACACCTGCCAATATCATATGAGTTCATA 1287
 QY 481 TCATTTCAGAGATGGGCACTTCCCTCAATGAATACAGATTAACATTCGGGAATTC 539
 Db 1288 TCATTTCAGAGATGGGCACTTCCCTCAATGAATACAGATTAACATTCGGGAATTC 1346

RESULT 11
 LOCUS RATIGFIA 1052 bp mRNA linear ROD 29-MAY-2002
 DEFINITION Rattus sp. mRNA for insulin-like growth factor I precursor.
 ACCESSION D00698
 VERSION D00698.1 GI:220780
 KEYWORDS Insulin-like growth factor I.
 SOURCE Rattus sp. liver cDNA to mRNA.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 28 to 1052)
 AUTHORS Shimatsu,A. and Rotwein,P.
 TITLE Mosaic evolution of the insulin-like growth factors. Organization, sequence, and expression of the rat insulin-like growth factor I gene.
 JOURNAL J. Biol. Chem. 262 (16), 7894-7900 (1987)
 MEDLINE 87222423
 REFERENCE 2 (bases 1 to 1052)
 AUTHORS Kato,H., Okoshi,A., Miura,Y. and Noguchi,T.
 TITLE A new cDNA clone relating to larger molecular species of rat insulin-like growth factor-I mRNA
 JOURNAL Agric. Biol. Chem. 54 (6), 1599-1601 (1990)
 MEDLINE 91103966
 COMMENT The difference in the size of IGF-I mRNA has been suggested to be primarily due to differences in the 3'-untranslated region in [1]. The cDNA clone to IGF-I mRNA reported in [2] gives direct evidence for this hypothesis.

FEATURES
 source location/Qualifiers
 1..1052
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 43..426

CDS

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FYFNKPTGSSIRAPQITVECCFRSDLRLEMYCAPLPTKSARSIRAPRHTD
MPKQKEVHLKNTSRGSGNKTYRM"
109..318
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606
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625
variation
/notes="c in [2]; a in [1]"
645
variation
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710..715
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731
polyA_site
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1023
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BASE COUNT      301 a      256 c      225 g      270 t
ORIGIN
Query Match      74.7%; Score 402.6; DB 10; Length 1052:
Best Local Similarity 88.5%; Pred. No. 1.2e-115;
Matches 470; Conservative 0; Mismatches 9; Indels 52; Gaps 1;
QY      1  GGACCAAGAGACCCCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 60
DB      109 GGACCAAGAGACCCCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 168
QY      61 AGGGGCTTTTCTTCAACAGCCACAGTCTATGGCTCCAGCATTCGAGGGCCACCA 120
DB      159 AGGGGCTTTTCTTCAACAGCCACAGTCTATGGCTCCAGCATTCGAGGGCCACCA 228
QY      121 ACGGGCATTTGTGATGAGTGTGCTCCGGAGCTGTATCTGAGAGAGCTGGAGATGTAC 180
DB      229 ACGGGCATTTGTGATGAGTGTGCTCCGGAGCTGTATCTGAGAGAGCTGGAGATGTAC 288
QY      181 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 240
DB      289 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 348
QY      241 ATGCCCAAGACTCAGAACTCCAGCCCTATCGACACACAGAAAGAAAGCTGCAAGG 300
DB      349 ATGCCCAAGACTCAG----- 363
QY      301 AGAAGGAAGAGAGTACACTTGAAGAACACAGTAGAGAAAGTGCAGAAACAGACCTA 360
DB      364 -----AAGGAAGTACACTTGAAGAACACAGTAGAGAAAGTGCAGAAACAGACCTA 416
QY      361 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATGCGACGTACCGCAAGATCCTTG 420
DB      417 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATGCGACGTACCGCAAGATCCTTG 476
QY      421 CTGCTTGAAGCAACCTGCAAAACATCGAAGACACTGCAAAATATCAATATATGAGTTCA 480
DB      477 CTGCTTGAAGCAACCTGCAAAACATCGAAGACACTGCAAAATATCAATATATGAGTTCA 536
QY      481 TCATTTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 531
DB      537 CCATTTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 587

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RESULT 12
RATGJTL      513 bp      mRNA      linear      ROD 27-APR-1993
LOCUS      Rat insulin-like growth factor-I mRNA, 3' end.
DEFINITION      M17714
ACCESSION      M17714.1 GI:204324
VERSION      M17714.1
KEYWORDS      Insulin-like growth factor.
SOURCE      Rat kidney, cDNA to mRNA.
ORGANISM      Rattus norvegicus

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Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae;
Rattus
REFERENCE      1 (bases 1 to 513)
AUTHORS      Murphy, L.J., Bell, G.I., Duckworth, M.L. and Friesen, H.G.
TITLE      Identification, characterization, and regulation of a rat
complementary deoxyribonucleic acid which encodes insulin-like
growth factor-I
JOURNAL      Endocrinology 121 (2), 684-691 (1987)
MEDLINE      87246437
PUBMED      3595538
FEATURES
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Location/Qualifiers
1..513
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<1..513
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CDS
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/notes="insulin-like growth factor-I signal peptide"
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mat_peptide
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BASE COUNT      143 a      128 c      135 g      107 t
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Query Match      74.4%; Score 401; DB 10; Length 513:
Best Local Similarity 88.3%; Pred. No. 3.4e-115;
Matches 469; Conservative 0; Mismatches 10; Indels 52; Gaps 1;
QY      1  GGACCAAGAGACCCCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 60
DB      10  GGACCAAGAGACCCCTTTGGGGGGCTGAGCTGTGAGCCCTCTTCACTTGTGTGACCA 69
QY      61 AGGGGCTTTTCTTCAACAGCCACAGTCTATGGCTCCAGCATTCGAGGGCCACCA 120
DB      70 AGGGGCTTTTCTTCAACAGCCACAGTCTATGGCTCCAGCATTCGAGGGCCACCA 129
QY      121 ACGGGCATTTGTGATGAGTGTGCTCCGGAGCTGTATCTGAGAGAGCTGGAGATGTAC 180
DB      130 ACGGGCATTTGTGATGAGTGTGCTCCGGAGCTGTATCTGAGAGAGCTGGAGATGTAC 189
QY      181 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 240
DB      190 TGTGCTCCGCTCAAGCCCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 249
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DB      250 ATGCCCAAGACTCAG----- 264
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DB      265 -----AAGGAAGTACACTTGAAGAACACAGTAGAGAAAGTGCAGAAACAGACCTA 317
QY      361 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATGCGACGTACCGCAAGATCCTTG 420
DB      318 CAGAAATGTAGAGAGAGCTCCCGAGAGAACAGAAATGCGACGTACCGCAAGATCCTTG 377
QY      421 CTGCTTGAAGCAACCTGCAAAACATCGAAGACACTGCAAAATATCAATATATGAGTTCA 480
DB      378 CTGCTTGAAGCAACCTGCAAAACATCGAAGACACTGCAAAATATCAATATATGAGTTCA 437
QY      481 TCATTTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 531
DB      438 CCATTTTCAGAGATGGGCAATTCCTCAATGAATATACACAGTAACATTC 488

```


RESULT 13
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 LOCUS Rat mRNA for insulin-like growth factor I (IGF-I).
 ACCESSION X06043.1 GI:56434
 VERSION X06043.1 GI:56434
 KEYWORDS Insulin-like growth factor I.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 521)
 AUTHORS Murphy, L.J., Bell, G.I., Duckworth, M.L. and Friesen, H.G.
 TITLE Identification, characterization, and regulation of a rat
 complementary deoxyribonucleic acid which encodes insulin-like
 growth factor-I
 JOURNAL Endocrinology 121 (2), 684-691 (1987)
 MEDLINE 87246437
 PUBMED 3595538
 COMMENT Data kindly reviewed (11-FEB-88) by Murphy L. J.
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 Best Local Similarity 88.3%; Pred. No. 3.4e-115;
 Matches 469; Conservative 0; Mismatches 10; Indels 52; Gaps 1;
 QY 1 GGACCAAGACCCCTTTCGGGGGCTGAGCTGTGAGCGCTCTTCACTTCTGTGTGACCA 60
 DB 10 GGACCAAGACCCCTTTCGGGGGCTGAGCTGTGAGCGCTCTTCACTTCTGTGTGACCA 69
 QY 61 AGGGGCTTTTACTTCAACAGCCCAAGTCTATGCTTCAGATTCGAGGGGACACAG 120
 DB 70 AGGGGCTTTTACTTCAACAGCCCAAGTCTATGCTTCAGATTCGAGGGGACACAG 129
 QY 121 ACGGGCATTTGTGATGTGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180
 DB 130 ACGGGCATTTGTGATGTGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 189
 QY 181 TGTTCGCTGACAGCTTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 240
 DB 190 TGTTCGCTGACAGCTTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 249
 QY 241 ATGCCCAAGACTCGAAGTCCAGCCCTTATGCACACACAAAGAAAGAGCTGCAAG 300
 DB 250 ATGCCCAAGACTCGAAGTCCAGCCCTTATGCACACACAAAGAAAGAGCTGCAAG 300
 QY 301 AGAAGAAAGAAAGTACACTTGAAGACACAGTGAAGAGAGTGAAGAAAGAAAGCTTA 360
 DB 265 AAGGAAGTACACTTGAAGACACAGTGAAGAGAGTGAAGAAAGAAAGAAAGCTTA 317

QY 361 CAGATGTAGAGAGAGGCTCCCGAGAACAGAAATGCCACGTCACCGAGACTCTTG 420
 DB 318 CAGATGTAGAGAGAGGCTCCCGAGAACAGAAATGCCACGTCACCGAGACTCTTG 377
 QY 421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCGCAATATCAATAGATTCA 480
 DB 378 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCGCAATATCAATAGATTCA 437
 QY 481 TCATTGAGAGAGGAGCTTCCCTCAATGAATACAGTAACATTC 531
 DB 438 CCATTGAGAGAGGAGCTTCCCTCAATGAATACAGTAACATTC 488

RESULT 14
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 LOCUS Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
 ACCESSION M17335.1 GI:204751
 VERSION M17335.1 GI:204751
 KEYWORDS Insulin-like growth factor I.
 SOURCE Rat (Sprague Dawley) testis, cDNA to mRNA, clone p2.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 826)
 AUTHORS Casella, S.J., Smith, E.P., van Wyk, J.J., Joseph, D.R., Hynes, M.A.,
 Hoyt, E.C. and Lund, P.K.
 TITLE Isolation of rat testis cDNAs encoding an insulin-like growth
 factor I precursor
 JOURNAL DNA 6 (4), 325-330 (1987)
 MEDLINE 88003970
 PUBMED 3652906
 FEATURES
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 259..642
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BASE COUNT 223 a 214 c 181 g 208 t
 ORIGIN
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 Best Local Similarity 88.0%; Pred. No. 9.7e-111;
 Matches 455; Conservative 0; Mismatches 10; Indels 52; Gaps 1;
 QY 1 GGACCAAGACCCCTTTCGGGGGCTGAGCTGTGAGCGCTCTTCACTTCTGTGTGACCA 60
 DB 325 GGACCAAGACCCCTTTCGGGGGCTGAGCTGTGAGCGCTCTTCACTTCTGTGTGACCA 384
 QY 61 AGGGGCTTTTACTTCAACAGCCCAAGTCTATGCTTCAGATTCGAGGGGACACAG 120
 DB 385 AGGGGCTTTTACTTCAACAGCCCAAGTCTATGCTTCAGATTCGAGGGGACACAG 444
 QY 121 ACGGGCATTTGTGATGTGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180
 DB 445 ACGGGCATTTGTGATGTGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 504
 QY 181 TGTTCGCTGACAGCTTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 240
 DB 505 TGTTCGCTGACAGCTTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 564
 QY 241 ATGCCCAAGACTCGAAGTCCAGCCCTTATGCACACACAAAGAAAGAGCTGCAAG 300
 DB 565 ATGCCCAAGACTCGAAGTCCAGCCCTTATGCACACACAAAGAAAGAGCTGCAAG 300

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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 09:07:57 ; Search time 163.509 Seconds

(without alignments)
7423.602 Million cell updates/sec

Title: US-09-852-261-3

Perfect score: 539
Sequence: 1 ggaccagagacccttgcg.....agtaaacctcccggaattc 539

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	100.0	539	22	AAD06399
2	539	100.0	539	24	AA016876
3	425	78.8	487	22	AA006404
4	425	78.8	487	24	AA016883
5	402.6	74.7	1052	20	AA027498
6	356.8	66.2	523	22	AA006400
7	356.8	66.2	523	24	AA016879
8	356.8	66.2	553	18	AA084893
9	325.2	60.3	517	22	AA006398

10	325.2	60.3	517	24	AA016877	Human mechano-grow
11	274.2	50.9	818	8	AA070436	Sequence encoding
12	274.2	50.9	7260	24	ABK84583	Human CDNA differe
13	274.2	50.9	7260	24	ABN97244	Gene #3742 used to
14	274.2	50.9	7260	24	ABK64812	Human benign prost
15	274.2	50.9	7260	24	ABK35504	Human endometrial
16	274.2	50.9	7260	24	ABK35561	Gene IGF1 differen
17	272.6	50.6	777	18	AA084894	Human insulin like
18	271	50.3	622	7	AA060490	Human prepro-somat
19	262	48.6	471	22	AAD06405	Rabbit liver-type
20	262	48.6	471	24	AA016884	Rabbit insulin-lik
21	231	42.9	1136	8	AA070435	Sequence encoding
22	230.2	42.7	978	14	AA047804	Sequence encoding
23	224	41.6	612	22	AA016895	Human CDNA encoding
24	222	41.2	3599	19	AAV50428	Plasmid pIG0552 lo
25	222	41.2	3599	19	AAV40796	Actual sequence of
26	222	41.2	3600	19	AAV50427	Plasmid pIG0552 up
27	222	41.2	3600	19	AAV40795	Expected sequence
28	222	41.2	5707	20	AA088055	Plasmid pIG0335 DN
29	222	41.2	6345	20	AA088054	Plasmid pIG0100A D
30	206.8	38.4	317	24	AA016882	Human insulin-like
31	206.8	38.4	318	22	AAD06403	Human liver-type I
32	206.8	38.4	462	19	AAV50426	Human IGF-1 encodi
33	206.8	38.4	462	19	AAV40794	Human IGF-1 coding
34	206.8	38.4	462	24	AB016999	Human polynucleoti
35	168.4	31.2	210	24	ABA03146	Native mature IGF-
36	166.8	30.9	237	12	AA013566	Human IGF-1 encodi
37	166.8	30.9	238	12	AA013566	Human IGF-1 encodi
38	166.8	30.9	2862	19	AA013566	Human IGF-1 encodi
39	165.2	30.6	207	22	AAH22139	Truncated human in
40	165.2	30.6	462	19	AAV50425	Human IGF-1 encodi
41	165.2	30.6	462	19	AAV40793	Human IGF-1 encodi
42	164.6	30.5	4532	24	AAD32015	Optimised IGF-1 co
43	163.6	30.4	210	24	AAD32016	Bovine alpha lacta
44	161.2	29.9	240	13	AA023303	Human insulin-like
45	161.2	29.9	390	18	AA063526	Synthetic human IG

ALIGNMENTS

RESULT 1	
ID	AAD06399 standard; CDNA: 539 BP.
XX	XX
AC	AAD06399;
XX	XX
DT	10-AUG-2001 (first entry)
XX	XX
DE	Rat IGF-I isoform mechano-growth factor (MGF) CDNA.
KW	Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW	mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW	amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW	polymyositis; post-polio syndrome; toxin; motoneurone disorder;
KW	nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW	sex-linked muscular dystrophy; peripheral neuropathy;
KW	Alzheimer's disease; Parkinson's disease; ss.
XX	XX
OS	Rattus sp.
XX	XX
FH	XX
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..336
FT	/*tag= a
FT	/product= "Mechano-growth factor (MGF)"
FT	/note= "This region comprises exons 3-6. The CDS does
FT	not include start codon"
FT	/partial
PN	MO200136483-AI.
XX	XX
XX	25-MAY-2001.
XX	XX

PF 15-NOV-2000; 2000MO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldslink G, Johnson I;
 XX
 DR WPI: 2001-355620/37.
 XX P-PSDB; AA02448.
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder.
 XX
 PS Claim 4: Page 51-52; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an insulin-like growth factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneuron loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneuron rescue, preferably adult motoneuron
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
 CC injury that affects motoneurons, motoneuron loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (EC) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.
 XX
 SQ Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;
 XX
 Query Match 100.0%; Score 539; DB 22; Length 539;
 Best Local Similarity 100.0%; Pred. No. 2,3e-142;
 Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 421 CTGCTTGGACCAACCTGGCAAAACATCGGACACCTGCCCAATATCAATGATTCATAA 480
 QY 481 TCATTTCAGAGATGGGCACTTTCCCTCAATGAATACCAAGTAACATTTCCGGAAATTC 539
 DB 481 TCATTTCAGAGATGGGCACTTTCCCTCAATGAATACCAAGTAACATTTCCGGAAATTC 539
 RESULT 2
 ID AAS16878
 ID AAS16878 standard; cDNA; 539 BP.
 AC AAS16878;
 XX
 XX 25-FEB-2002 (first entry)
 DT
 DE Rat mechano-growth factor (MGF) cDNA.
 XX
 KM Rat: mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KM neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KM muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KM nerve avulsion.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT 1..336
 FT CDS /tag= a
 FT /product= "Rat MGF"
 FT /partial
 FT /note= "No start codon"
 FT 1..75
 FT /tag= b
 FT /number= exon 3
 FT 76..258
 FT /tag= c
 FT /number= exon 4
 FT 259..309
 FT /tag= d
 FT /number= exon 5
 FT 310..333
 FT /tag= e
 FT /number= exon 6
 XX
 PN MO200185781-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001MO-GB02054.
 PR 10-MAY-2000; 2000GB-0011278.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
 XX
 PI Goldslink G, Terenghi G;
 XX
 DR WPI: 2002-055685/07.
 DR P-PSDB; AAU10560.
 XX
 PT Use of insulin-like growth factor I (IGF-I) isoform known as
 PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
 PT ability to reduce motoneuron loss in response to nerve avulsion, to
 PT treat nerve damage.
 XX
 PS Disclosure: Fig 6; 65pp; English.
 XX
 CC The invention relates to the use of an insulin-like growth factor I
 CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
 CC of a medicament for treating nerve damage in the peripheral nervous
 CC system, or for treating nerve damage by localising MGF at the site of
 CC damage. The nerve damage may include severing of a nerve. The treatment
 CC may be combined with another treatment (such as a polypeptide growth

factor other than MGF that prevents or diminishes degeneration of the target organ (for example, muscle) which the damaged nerve innervates, whereby the treatment of the muscle with MGF or a polynucleotide encoding MGF prevents or diminishes degeneration. The method is useful for treating neurological disorders, preferably motoneuron disorders. These conditions can reduce motoneuron loss by 20% or greater in response to nerve avulsion. This sequence represents cDNA encoding the rat MGF.

Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 100.0%; Score 539; DB 24; Length 539;
Best Local Similarity 100.0%; Pred. No. 2,3e-142;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGACACAGAGACCTTTGGGGGGGTGAGTGTGAGAGCTCTTCACTGTGTGTGACCA 60
1 GGACACAGAGACCTTTGGGGGGGTGAGTGTGAGAGCTCTTCACTGTGTGTGACCA 60
61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGCTCCAGATTGGAAGGACACAG 120
61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGCTCCAGATTGGAAGGACACAG 120
121 ACAGGCAATGTGTGATGATGTTGCTTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180
121 ACAGGCAATGTGTGATGATGTTGCTTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180
181 TGTGTCCGCTGCAAGCTTCAAAAGTACGCTTCCATCCGGGCCACGACACTGAC 240
181 TGTGTCCGCTGCAAGCTTCAAAAGTACGCTTCCATCCGGGCCACGACACTGAC 240
241 ATGCCCAAGACTAGAGTCCAGAGCCCTATGACACACAAAGAAAGAGTGCAGAG 300
241 ATGCCCAAGACTAGAGTCCAGAGCCCTATGACACACAAAGAAAGAGTGCAGAG 300
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301 AGAAGAAAGAAAGTACACTTGAAGAACAAAGTGAAGAAAGTGAAGAAAGTGA 360
361 CAGAAATGTAGAGAGACCTCCGAGAGACAGAAATGCTCCAGAGATCTTTG 420
361 CAGAAATGTAGAGAGACCTCCGAGAGACAGAAATGCTCCAGAGATCTTTG 420
421 CTGCTTGAAGACCTGCAAAACATCGGACACCTGCAAAATGCAATATGATGATCA 480
421 CTGCTTGAAGACCTGCAAAACATCGGACACCTGCAAAATGCAATATGATGATCA 480
481 TCATTTGAGAGATGGGCAATTTCCCTCAATGAATACACAGTAATCATTCGGAATTC 539
481 TCATTTGAGAGATGGGCAATTTCCCTCAATGAATACACAGTAATCATTCGGAATTC 539

RESULT 3
AAD06404
ID AAD06404 standard; cDNA; 487 BP.

AC AAD06404;
XX 10-AUG-2001 (first entry)

DE Rat liver-type IGF-I isoform (L-IGF-I) cDNA.

Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
mechano-growth factor; neurological disorder; neurodegenerative disorder;
amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
polymyositis; post-polio syndrome; toxin; motoneuron disorder;
nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
sex-linked muscular dystrophy; peripheral neuropathy;
Alzheimer's disease; Parkinson's disease; liver; L-IGF-I; ss.

Rattus sp.
XX Key Location/Qualifiers
XX CDS 1..318

/tag- a "liver-type IGF-I isoform (L-IGF-I)"
/product- a "liver-type IGF-I isoform (L-IGF-I)"
/transl- except- (pos:304..306, aa:1-10)
/note- "The translation exception occurs while decoding the alternative version of the protein (AAE02531). The CDS comprises exons 3, 4 and 6 and does not include start codon"

W0200136483-A1.

25-MAY-2001.

15-NOV-2000; 2000MO-GB04354.

15-NOV-1999; 99GB-0026968.

(UNLO) UNIV COLLEGE LONDON.

Goldspink G, Johnson I;

WPI; 2001-355620/37.

P-PSDB: AAE02451, AAE02531.

Use of mechano-growth factor, an isoform of Insulin-like Growth Factor-I, capable of reducing motoneuron loss, in the manufacture of a medicament for the treatment of neurological disorder

Disclosure; Page 57-58; 66pp; English.

The present invention relates to use of mechano-growth factor (MGF), an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a medicament for the treatment of neurological disorder. The MGF is capable of reducing motoneuron loss by 20% or greater in response to nerve avulsion and effects motoneuron rescue, preferably adult motoneuron rescue. The MGF polynucleotide and polypeptide are useful in the manufacture of a medicament for the treatment of a neurological disorder, including a disorder of motoneurons and/or neurodegenerative disorder, e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive spinal muscular atrophy, infantile or juvenile muscular atrophy, CC polymyositis or post-polio syndrome, a disorder caused by exposure to a toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an injury that affects motoneurons, motoneuron loss associated with aging, autosomal or sex-linked muscular dystrophy, diabetic neuropathy, CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease. The present sequence is rat liver-type IGF-I isoform (L-IGF-I) cDNA. The L-IGF-I protein comprises amino acid sequences encoded by nucleic acid sequence of IGF-I exons 4 and 6.

Sequence 487 BP; 139 A; 123 C; 126 G; 99 T; 0 other;

Query Match 78.8%; Score 425; DB 22; Length 487;
Best Local Similarity 90.4%; Pred. No. 3.5e-110;
Matches 487; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

1 GGACACAGAGACCTTTGGGGGGGTGAGTGTGAGAGCTCTTCACTGTGTGTGACCA 60
1 GGACACAGAGACCTTTGGGGGGGTGAGTGTGAGAGCTCTTCACTGTGTGTGACCA 60
61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGCTCCAGATTGGAAGGACACAG 120
61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGCTCCAGATTGGAAGGACACAG 120
121 ACAGGCAATGTGTGATGATGTTGCTTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180
121 ACAGGCAATGTGTGATGATGTTGCTTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180
181 TGTGTCCGCTGCAAGCTTCAAAAGTACGCTTCCATCCGGGCCACGACACTGAC 240
181 TGTGTCCGCTGCAAGCTTCAAAAGTACGCTTCCATCCGGGCCACGACACTGAC 240
241 ATGCCCAAGACTAGAGTCCAGAGCCCTATGACACACAAAGAAAGAGTGCAGAG 300

KW diabetic; ss.
 XX
 OS Rattus sp.
 XX
 PN W0910013-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 25-AUG-1998; 98WO-US17428.
 XX
 PR 25-AUG-1997; 97US-0057201.
 XX
 PA (MASC-) MASSACHUSETTS GEN HOSPITAL.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Rosenthal NA, Sweeney HL;
 XX
 DR WPI; 1999-190469/16.
 XX
 PT Use of modified insulin-like growth factor I - in gene therapy for
 PT increasing vertebrate muscle strength and mass
 PS
 PS Example 1; Fig 4; 46pp; English.
 CC This sequence represents the liver isoform of the rat insulin-like
 CC growth factor I (IGF-I) from rats. IGF-I or a modified or biologically
 CC active portion can be used for increasing vertebrate muscle mass by
 CC intramuscular administration, for e.g. (i) preserving or enhancing
 CC muscle strength in aging humans; (ii) healing injured muscle more
 CC efficiently/rapidly; (iii) controlling muscle mass during disease and/or
 CC prolonged stays in reduced gravity; (iv) cosmetic body sculpting; and
 CC (v) promoting glucose clearance from diabetic muscle tissue.
 XX
 XX Sequence 1052 BP; 301 A; 256 C; 225 G; 270 T; 0 other;
 SQ
 Query Match 74.7%; Score 402.6; DB 20; Length 1052;
 Best Local Similarity 88.5%; Pred. No. 9.8e-104;
 Matches 470; Conservative 0; Mismatches 9; Indels 52; Gaps 1;
 QY 1 GGACCGAGAGACCCCTTGGCGGGCTGAGCTGTGAGCGCTTCAGTTGTGTGAGACA 60
 DB 109 GGACCGAGAGACCCCTTGGCGGGCTGAGCTGTGAGCGCTTCAGTTGTGTGAGACA 168
 QY 61 AGGGGCTTTACTTCAACAGGCCACAGCTATGCTCCAGCATTCGGAGGGCCACACAG 120
 DB 169 AGGGGCTTTACTTCAACAGGCCACAGCTATGCTCCAGCATTCGGAGGGCCACACAG 228
 QY 121 ACGGGCATTTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGGAGCGCTGGAGATGTAC 180
 DB 229 ACGGGCATTTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGGAGCGCTGGAGATGTAC 288
 QY 181 TGTGTCCGCTGCAAGCTTCAAGTCACTGCTTCATCCGGGCCACGGCCACACTGAC 240
 DB 289 TGTGTCCGCTGCAAGCTTCAAGTCACTGCTTCATCCGGGCCACGGCCACACTGAC 348
 QY 241 ATGCCCAAGACTCAGAGTCCAGCCCTATCGACACACAGAAAGAAAGAACTCCAAAG 300
 DB 349 ATGCCCAAGACTCAGAGTCCAGCCCTATCGACACACAGAAAGAAAGAACTCCAAAG 363
 QY 301 AGAAGAAAGAGAGTACACTTGAAGACACAGTAGAGAGAGTCCAGGAACAGACCTTA 360
 DB 364 -----AAGAGAGTACACTTGAAGAGACACAGTAGAGAGTCCAGGAACAGACCTTA 416
 QY 361 CAGAAATGAGAGAGAGTCCCGGAGAGACAGAAATGCCAGTACCGCAAGATCTTTG 420
 DB 417 CAGAAATGAGAGAGAGTCCCGGAGAGACAGAAATGCCAGTACCGCAAGATCTTTG 476
 QY 421 CTGCTTGAACAACCTGCAAAAACATCGGAACACTGCCAAATATCAATATGAGTTCAATA 480
 DB 477 CTGCTTGAACAACCTGCAAAAACATCGGAACACTGCCAAATATCAATATGAGTTCAATA 536
 QY 481 TCATTTCAGAGATGGGCAATTCCTCCTCAATGAATACACAGTAACATTC 531
 XX

DB 537 CCATTTCAGAGATGGGCAATTCCTCCTCAATGAATACACAGTAACATTC 587
 RESULT 6
 AAD06400
 ID AAD06400 standard; CDNA: 523 BP.
 XX
 AC AAD06400;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Rabbit IGF-I isoform mechano-growth factor (MGF) CDNA.
 XX
 KW Rabbit; IGF-I isoform; insulin-like Growth Factor-I; MGF;
 KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
 KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
 KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; ss.
 XX
 OS Oryctolagus cuniculus.
 XX
 FH Key Location/Qualifiers
 FT 1..336
 FT CDS /tag= a
 FT /product= "Mechano-growth factor (MGF)"
 FT /note= "This region comprises exons 3-6. The CDS does
 FT not include start codon"
 FT /partial
 XX
 PN W0200136483-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldsprint G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 XX
 P-PSDB: AAE02449.
 XX
 PT Use of mechano-growth factor, an isoform of insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder.
 XX
 PS Claim 4; Page 53-54; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (EC) domain, hence also referred as
 CC IGF-1-EC. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.
 XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 66.2%; Score 356.8; DB 22; Length 523;
Best Local Similarity 82.3%; Pred. No. 6,7e-91;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

QY 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGGAGCCA 60
DB 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGGAGCCA 60
QY 61 AGGGGCTTTTACTTCAACAAAGCCACAGTATGCTCCAGCATTCGGAGGACCAAG 120
DB 61 AGGGGCTTTTACTTCAACAAAGCCACAGTATGCTCCAGCATTCGGAGGACCAAG 120
QY 121 ACAGGCAATTTGATGATGATGCTTCCGAGGCTGATGTAGAGGAGGCTGGAGATGAC 180
DB 121 ACAGGCAATTTGATGATGATGCTTCCGAGGCTGATGTAGAGGAGGCTGGAGATGAC 180
QY 181 TGTGTCGGCTGCAAGCTTACAAAGTACGCTGCTTCATCCGGGGCCAGCCCACTGAC 240
DB 181 TGTGTCGGCTGCAAGCTTACAAAGTACGCTGCTTCATCCGGGGCCAGCCCACTGAC 240
QY 241 ATGCCCAAGACTCGAAGTCCCAAGCCCTATGCAACACAAAGAAAGAGCTGCAAG 300
DB 241 ATGCCCAAGACTCGAAGTCCCAAGCCCTATGCAACACAAAGAAAGAGCTGCAAG 300
QY 301 AGAAGGAAGGAAGTACCTTGAAGAACACACAGTAGAGAGTGCAGAAACAGACTA 360
DB 301 AGAAGGAAGGAAGTACCTTGAAGAACACACAGTAGAGAGTGCAGAAACAGACTA 360
QY 361 CAGATATAGAGAGAGCTCCCGCAGACAGCAAAATGCCAGCTCCAGCATCTTTG 420
DB 361 CAGATATAGAGAGAGCTCCCGCAGACAGCAAAATGCCAGCTCCAGCATCTTTG 420
QY 421 CTGCTTGAGCAACCTGCAACATCCGACACCTGCAATATCATTAATGATTTCAATA 480
DB 421 CTGCTTGAGCAACCTGCAACATCCGACACCTGCAATATCATTAATGATTTCAATA 480
QY 481 TCATTTGAGAGAGGAGCTTCCCTCAATGAATATACACAGTAACATTC 530
DB 481 TCATTTGAGAGAGGAGCTTCCCTCAATGAATATACACAGTAACATTC 530
QY 475 ACATTTCAAGAT-GGCATTTTCCCAATGAATATACACAGTAACATTC 523
DB 475 ACATTTCAAGAT-GGCATTTTCCCAATGAATATACACAGTAACATTC 523

RESULT 7

AA16879 ID AAS16879 standard; cDNA; 523 BP.

XX AAS16879;

XX 25-FEB-2002 (first entry)

XX Rabbit mechano-growth factor (MGF) cDNA.

XX Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
XX neuroprotective; nerve damage; peripheral nervous system; nerve severing;
XX muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
XX nerve avulsion.

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers

XX CDS 1..336

XX FT /tag= a

XX FT /product= "Rabbit MGF"

XX FT /partial

XX FT /note= "No start codon"

XX FT 1..76

XX FT /tag= b

XX FT /number= 3

XX FT 77..259

XX FT /tag= c

XX FT /number= 4

XX FT 260..309

FT /tag= d
FT /number= 5
FT 311..333
FT /tag= e
FT /number= 6

PN MO200185781-A2.

PD 15-NOV-2001.

PE 10-MAY-2001; 2001WO-GB02054.

PR 10-MAY-2000; 2000GB-0011278.

PA (UNLO) UNIV COLLEGE LONDON.

PI (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

PI Goldslink G, Terenghi G;

DR WPI: 2002-055585/07.

DR P-PSDB: AAI10561.

PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage

PS Disclosure: Fig 7; 65pp; English.

CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates;
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motoneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit MGF.

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 66.2%; Score 356.8; DB 24; Length 523;
Best Local Similarity 82.3%; Pred. No. 6,7e-91;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

QY 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGGAGCCA 60
DB 1 GGACCCAGAGACCCCTTGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGGAGCCA 60
QY 61 AGGGGCTTTTACTTCAACAAAGCCACAGTATGCTCCAGCATTCGGAGGACCAAG 120
DB 61 AGGGGCTTTTACTTCAACAAAGCCACAGTATGCTCCAGCATTCGGAGGACCAAG 120
QY 121 ACAGGCAATTTGATGATGATGCTTCCGAGGCTGATGTAGAGGAGGCTGGAGATGAC 180
DB 121 ACAGGCAATTTGATGATGATGCTTCCGAGGCTGATGTAGAGGAGGCTGGAGATGAC 180
QY 181 TGTGTCGGCTGCAAGCTTACAAAGTACGCTGCTTCATCCGGGGCCAGCCCACTGAC 240
DB 181 TGTGTCGGCTGCAAGCTTACAAAGTACGCTGCTTCATCCGGGGCCAGCCCACTGAC 240
QY 241 ATGCCCAAGACTCGAAGTCCCAAGCCCTATGCAACACAAAGAAAGAGCTGCAAG 300
DB 241 ATGCCCAAGACTCGAAGTCCCAAGCCCTATGCAACACAAAGAAAGAGCTGCAAG 300
QY 301 AGAAGGAAGGAAGTACCTTGAAGAACACACAGTAGAGAGTGCAGAAACAGACTA 360
DB 301 AGAAGGAAGGAAGTACCTTGAAGAACACACAGTAGAGAGTGCAGAAACAGACTA 360

QY 361 CAAATGTGTGAGAGACCTCCCGAGAGAACAGAAATGTAGCTACCCGAAATCCTTG 420

Db 361 CAGAGATGTGAGAAAGACCTCTTGAGAGAGTGAAGAAAGACAGCCACCCGACAGACCTTTG 420

QY 421 CTGCTTGAGCAACCTGSCAAACATATGAGAAACACCTGCCAATATATTAATATGATGTCATA 480

Db 421 CTGTGCACAGTTACCTCTGTAAACATTTGAGATATCCGGCCGCA-----AAAATATAGTTGATC 474

QY 481 TCATTTTCAGAGATGGCATTTTCCCTCAATGAATATACACAGATAACAATTC 530

Db 475 ACATTTTCAAGAT-GGCATTTTCCCCCAATGAAATATCAACAATTAACATTC 523

RESULT	8
AAT84893	
ID	AAT84893 standard; cDNA; 553 bp
XY	

DT 14-APR-1998 (first entry)
XY

Rabbit insulin like growth factor 1 encoding cDNA

KW Insulinlike growth factor 1; IGF-1; Ec peptide; muscle disorder
KW heart; neuromuscular disease; primer; ss.
XX

Oryctolagus cuniculus.

FH	Key	Location/Qualifiers
EE	CDC	1-300

product= "IGF-1"

PN W09733997-A1

PD 18-SEP-1997

11-MAR-1997; 97WO-GB00658

PR 11-MAR-1996; 96GB-0005124.

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

Goldspink G;

DR WPI; 1997-470877/43.

XX

PT peptide - to

[illegible]

PS Disclosure; Fig 3; 33pp; English.

CC A use of insulin like growth factor I (IGF-1) has been developed, and

CC equivalent, in the treatment or therapy of a human or animal. The IGF-1

Becker muscular dystrophy, autosomal dystrophies and related progressive

spinal cord injury induced muscle atrophy and neuromuscular diseases.

and cardiac disorders, e.g. diseases where promotion of cardiac muscle protein synthesis is a beneficial treatment, cardiomyopathies and acute

infarction. It can also be used to promote bone fracture healing and

CC maintenance of bone in old age. The present sequence encodes rabbit
CC IGF-1 used in the present specification.

Sequence 553 BP: 159 A: 142 C: 147 G: 105 T: 0 other:

Query Match	66.2%;	Score 356.8;	DB 18;	Length 553;
Best Local Similarity	82.3%;	Pred. No. 6.8e-91;		
Matches 436;	Conservative 0;	Mismatches 87;	Indels 7;	Gaps 2;

QY	1	GGACCAAGAGACCCCTTTGGGGGGCTGAGCTGAGTGGAGAGCGCTTCACCTAGTGTGTGGAGCA	60
Db	31	GGACCGGAGAGCGCTCTGCGGTGTGTGAGCTGGTGATGCTCTTCACATTTGTGTGGAGAC	90
QY	61	AGGGCGCTTTTACTTCAACAAGCCGACAGTCTATGGCTCCAGCATTCGGAGGGCACACAG	120
Db	91	AGGGCGCTTTTATTTCACAAGCCGACAGGATACGGCTCCAGCAGTCTGGAGGGCACCTCAG	150
QY	121	ACGGGCAATTGGATGAGTGGTTGCTTCGCGAGACTGATCGAGGAGGCTGGAAATATAC	180
Db	151	ACAGGCACTCGTGGATGAGTGTCTCTTCGCGAGCTGTGATCTGGAGGCTGGAAATATGAC	210
QY	181	TGTGTCCGCTGCAGACCTACAAAGTCAAGCTCGTTCATCCGAGGCCACGCGACACTGAC	240
Db	211	TGTGCACCCCTCAAGCGCGGAAAGGACGCGCCCTCGGTCGGCCACGCGCACACCGAC	270
QY	241	ATGGCCCAAGACTAGAAAGTCCGACCCCTATGACACACAGAAAGAAAGAACTCCAAAG	300
Db	271	ATGGCCCAAGACTAGAAAGTATCGCTCCATCTACCAACAGAAATATAACTCTCAAGG	330
QY	301	AGAAGAAAGAAAGTACACTTGAAGACACAAGTAGAGAAAGTCAGAGAAACAAGACTTA	360
Db	331	AGAAGAAAGAAAGTACACTTGAAGACACAAGTAGAGAAAGTCAGAGAAACAAGACTTA	390
QY	361	CAGATATAGSAGSAGGCTCCGAGSAGACAGAAATGCCACGTACCGCAAGATCCTTG	420
Db	391	CAGATATAGSAGSAGGCTCTTGAGSAGTGAAGAAAGGACAGGACCGCAGGACCCCTTG	450
QY	421	CTGGTTGAGAACCTCCAAACATCGAAGACACTCCCAATATCAATATGAGTTCATA	480
Db	451	CTGGTCACAGTACTGTAAACATTGGAAATACCGGCCA-----AAAAATAGTTTATC	504
QY	481	TCATTTCAAGATGGGCATTTCCCTCATGAATACCAAGTAACATTC	530
Db	505	ACATTTCAAGAT--GGCATTTTCCCAATGAATACCAAGTAACATTC	553

RESULT 9
AAD06398
ID AAD06398 standard; cDNA; 517 BP.

AC AAD06398;

DT 10-AUG-2001 (first entry)

DE Human IGF-I isoform mechano-growth factor (MGF) cDNA

KW Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

Alzheimer's disease; Parkinson's disease; ss.

Homo sapiens

FH	Key	Location/Qualifiers

3
1.000
/*tad=
/

/note" "This region comprises exons 3-6. The CDS does

not included
ET

AA
PN W0200136483-A1

AA PD 25-MAY-2001

AA
PF 15-NOV-2000: 2000WO-GB04354

AA 15-NOV-1999: 99GB-0026968
PR

XX (UNLO) UNIV COLLEGE LONDON.
PA Goldslink G, Johnson I;
XX WPI: 2001-355620/37.
XX P-PSDB: AAE02447.

DR Use of mechano-growth factor, an isoform of insulin-like growth
PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a
PT medicament for the treatment of neurological disorder.
XX
XX
PS Claim 4; Page 49-50; 66pp; English.

XX The present invention relates to use of mechano-growth factor (MGF),
CC an insulin-like growth factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneuron loss by 20% or greater in response to nerve
CC avulsion, and effects motoneuron rescue, preferably adult motoneuron
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurons and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy, progressive
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
CC injury that affects motoneurons, motoneuron loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (EC) domain, hence also referred as
CC IGF-I-EC. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.
XX
XX

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other:

Query Match 60.3%; Score 325.2; DB 22; Length 517;
Best Local Similarity 81.2%; Pred. No. 5; Gc-82;
Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

QY 1 GGACCCAGAGACCCCTTTCGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGAGACCA 60
DB 1 GGACCCAGAGACCCCTTTCGGGGGCTGAGCTGTGAGACCTCTTCACTGCTGTGAGACCA 60
QY 61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGCTCCAGATTCGGAGGCCACCAAG 120
DB 61 AGGGGCTTTTACTTCAACAAGCCCAAGCTATGCTCCAGATTCGGAGGCCACCAAG 120
QY 121 ACGGCGATTTGATGATGATGCTTCCGAGAGCTGATGATGAGAGGCTGGAGATGAC 180
DB 121 ACGGCGATTTGATGATGATGCTTCCGAGAGCTGATGATGAGAGGCTGGAGATGAC 180
QY 181 TGTGTCCGCTGACCTTCAACAAGCTGCTGTGATCCAGGCGCCGCACTGAC 240
DB 181 TGTGTCCGCTGACCTTCAACAAGCTGCTGTGATCCAGGCGCCGCACTGAC 240
QY 241 ATGCCCAAGACTAGAGTCCGAGCCCTATGACACACAGAAAGAGAGCTGCAAG 300
DB 241 ATGCCCAAGACTAGAGTCCGAGCCCTATGACACACAGAAAGAGAGCTGCAAG 300
QY 301 AGAAGGAAGGAAGTCACTTGAAGAACAACAAGTAGAGAGTGCAGAAACAAGACTA 360
DB 301 AGAAGGAAGGAAGTCACTTGAAGAACAACAAGTAGAGAGTGCAGAAACAAGACTA 360
QY 361 CAGAATGTAGAGAGCTCCGAGAGACAGAAATGCCACGTCACCCGAAGTCTTGG 420
DB 361 CAGAATGTAGAGAGCTCCGAGAGACAGAAATGCCACGTCACCCGAAGTCTTGG 420
QY 421 CTCTGCACAGTACCTGTAACATTTGAAATATACCGGCCA-----AAATAATAGTTTGAAC 480
DB 421 CTCTGCACAGTACCTGTAACATTTGAAATATACCGGCCA-----AAATAATAGTTTGAAC 480
QY 470
DB 470

QY 481 TCATTTCAGAGAGGCGCATTTCCCTCATGAAATACCAAGTAACAT 528
DB 471 ACATTTCAGAGAT-GGCATTTCCCAATGAATAACAGTAACAT 517

RESULT 10

AA516877
ID AA516877 standard; cDNA; 517 BP.
XX
AC AA516877;
XX
DT 25-FEB-2002 (first entry)
XX

DE Human mechano-growth factor (MGF) cDNA.

XX Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
XX nerve avulsion.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 1..333

FT /tag= a

FT /product= "Human MGF"

FT /partial

FT /note= "No start codon"

FT /tag= b

FT /number= 3

FT /tag= c

FT /number= 4

FT /tag= d

FT /number= 5

FT /tag= e

FT /number= 6

PN MO200185781-A2.

PD 15-NOV-2001.

XX 10-MAY-2001; 2001MO-GB02054.

PR 10-MAY-2000; 2000GB-0011278.

XX (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX Goldslink G, Terenghi G;

PI WPI: 2002-055585/07.

DR P-PSDB: AAU10559.

XX Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage

XX Claim 11; Fig 5; 65pp; English.

XX The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding

CC MGF prevents or diminishes degeneration. The method is useful for
 CC treating neurological disorders, preferably motor neuron disorders. These
 CC methods can reduce locomotion loss by 20% or greater in response to nerve
 CC avulsion. This sequence represents cDNA encoding the human MGF.

XX Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 60.3%; Score 325.2; DB 24; Length 517;
 Best Local Similarity 81.2%; Pred. No. 5,6e-82;
 Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

QY 1 GGACGAGAGACCCCTTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGCA 60
 1 GGACCGGAGAGCGCTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGCA 60
 QY 61 AGGGGCTTTTATTTTCAACAAGCCACAGAGTGTGCTCCAGATTCGAGGGCCACACAG 120
 61 AGGGGCTTTTATTTTCAACAAGCCACAGAGTGTGCTCCAGATTCGAGGGCCACACAG 120
 QY 121 ACAGGATGTGAGATGATGTTGCTCCGAGCTGTGATCTGAGGAGGCTGAGATGTAC 180
 121 ACAGGATGTGAGATGATGTTGCTCCGAGCTGTGATCTGAGGAGGCTGAGATGTAC 180
 QY 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGGGCCACGACACTGAC 240
 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGGGCCACGACACTGAC 240
 QY 241 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 300
 241 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 300
 QY 241 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 300
 241 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 300
 QY 301 AGAAGAAAGAGAGTACCTTGAAGACAGACAGTAGAGAGAGTGCAGAGAAACAGACTA 360
 301 AGAAGAAAGAGAGTACCTTGAAGACAGACAGTAGAGAGAGTGCAGAGAAACAGACTA 360
 QY 298 AGAAGAAAGAGAGTACCTTGAAGACAGACAGTAGAGAGAGTGCAGAGAAACAGACTA 357
 298 AGAAGAAAGAGAGTACCTTGAAGACAGACAGTAGAGAGAGTGCAGAGAAACAGACTA 357
 QY 361 CAGATGTAGAGAGAGCTCCCGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 420
 361 CAGATGTAGAGAGAGCTCCCGAGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 420
 QY 358 CAGATGTAGAGAGAGCTCCCGAGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 416
 358 CAGATGTAGAGAGAGCTCCCGAGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 416
 QY 421 CTGCTTGAGCAACCTGCAAAACATGGAACACCTGCAAAATATCAATATGATGATCA 480
 421 CTGCTTGAGCAACCTGCAAAACATGGAACACCTGCAAAATATCAATATGATGATCA 480
 QY 417 CTCTCAGACAGTACCTGTAAACATGGAATACCGGCCA-----AAAATAAGTTTATC 470
 417 CTCTCAGACAGTACCTGTAAACATGGAATACCGGCCA-----AAAATAAGTTTATC 470
 QY 481 TCATTTGAGAGATGGGCAATTTCCCTCATGGAATACCAAGTAACAT 528
 481 TCATTTGAGAGATGGGCAATTTCCCTCATGGAATACCAAGTAACAT 528
 QY 471 ACATTTCAAGAT-GGCATTTTCCCCCAATGAATACAGAAATTAACAT 517
 471 ACATTTCAAGAT-GGCATTTTCCCCCAATGAATACAGAAATTAACAT 517

RESULT 11
 AAN70436
 ID AAN70436 standard; cDNA; 818 BP.

AC AAN70436;
 DT 05-APR-1991 (first entry)

DE Sequence encoding insulin-like growth factor 1A (IGF-1A).

XX Growth promoter; lactation enhancer; cell proliferation; ss.

XX Homo sapiens.

XX EP229750-A.

XX 22-JUL-1987.

XX 06-JAN-1987; 87EP-0870001.

XX 20-NOV-1986; 86US-0928671.

XX 07-JAN-1986; 86US-0816662.

XX (UNIT) UNIV OF WASHINGTON.

PI Kriivi GG, Rotwein PS;
 XX WPI; 1987-200203/29.

PT New pre-insulin-like growth factor-1 protein - obtd. by
 PT recombinant DNA procedures for use as growth promoters for
 PT enhancing lactation, for stimulating cell proliferation etc.

XX Example; Fig 5; 59pp; English.

CC A 42 base oligonucleotide corresponding to the DNA sequence encoding
 CC amino acids 10 to 23 of mature human IGF-1 was synthesized (AAN70437).
 CC The radiolabeled 42 mer was then employed to screen for IGF-1
 CC containing DNA sequences in a human liver cDNA library. Insulin-
 CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA
 CC library by using lambda phage 11 (AAN70435, AAN70436). The human IGF-1
 CC genomic gene was isolated and mapped. It encodes at least two
 CC preproinsulin-like growth factor-1 proteins. An essentially pure
 CC preproinsulin-like growth factor-1 protein comprising the sequence
 CC of amino acids shown in Figure six is claimed (AAN70277).

SQ Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 50.9%; Score 274.2; DB 8; Length 818;
 Best Local Similarity 76.0%; Pred. No. 1.7e-67;
 Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

QY 1 GGACGAGAGACCCCTTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGCA 60
 1 GGACGAGAGAGAGCTCTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGCA 60
 QY 203 GGACGAGAGAGAGCTCTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGCA 262
 203 GGACGAGAGAGAGCTCTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGCA 262
 QY 61 AGGGGCTTTTATTTTCAACAAGCCACAGAGTGTGCTCCAGATTCGAGGGCCACACAG 120
 61 AGGGGCTTTTATTTTCAACAAGCCACAGAGTGTGCTCCAGATTCGAGGGCCACACAG 120
 QY 263 AGGGGCTTTTATTTTCAACAAGCCACAGAGTGTGCTCCAGATTCGAGGGCCACACAG 322
 263 AGGGGCTTTTATTTTCAACAAGCCACAGAGTGTGCTCCAGATTCGAGGGCCACACAG 322
 QY 121 ACAGGATGTGAGATGATGTTGCTCCGAGCTGTGATCTGAGGAGGCTGAGATGTAC 180
 121 ACAGGATGTGAGATGATGTTGCTCCGAGCTGTGATCTGAGGAGGCTGAGATGTAC 180
 QY 323 ACAGGATGTGAGATGATGTTGCTCCGAGCTGTGATCTGAGGAGGCTGAGATGTAC 382
 323 ACAGGATGTGAGATGATGTTGCTCCGAGCTGTGATCTGAGGAGGCTGAGATGTAC 382
 QY 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGGGCCACGACACTGAC 240
 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGGGCCACGACACTGAC 240
 QY 383 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGGGCCACGACACTGAC 442
 383 TGTGTCGCTGCAAGCTTCAAAAGTCAAGCTGCTCCATCCGGGCCACGACACTGAC 442
 QY 241 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 300
 241 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 300
 QY 443 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 457
 443 ATGCCCAAGACTCAGAGTCCAGCCCTATGCAACACAAAGAAAGAGTGCAGAGG 457
 QY 301 AGAAGAAAGAGAGTACCTTGAAGACAGACAGTAGAGAGAGTGCAGAGAAACAGACTA 360
 301 AGAAGAAAGAGAGTACCTTGAAGACAGACAGTAGAGAGAGTGCAGAGAAACAGACTA 360
 QY 458 -----AAGGAAGTACATTTGAAGAGAGAGTGCAGAGAAACAGACTA 510
 458 -----AAGGAAGTACATTTGAAGAGAGAGTGCAGAGAAACAGACTA 510
 QY 361 CAGATGTAGAGAGAGCTCCCGAGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 420
 361 CAGATGTAGAGAGAGCTCCCGAGAGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 420
 QY 511 CAGATGTAGAGAGAGCTCCCGAGAGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 570
 511 CAGATGTAGAGAGAGCTCCCGAGAGAGAGACAGAAATGCCAGTCCAGCCAGATCTTTG 570
 QY 421 --CTGCTTGAGCAACCTGCAAAACATGGAACACCTGCAAAATATCAATATGATGATCA 478
 421 --CTGCTTGAGCAACCTGCAAAACATGGAACACCTGCAAAATATCAATATGATGATCA 478
 QY 571 CTCTCAGACAGTACCTGTAAACATGGAATACCGGCCA-----AAAATAAGTTTGA 624
 571 CTCTCAGACAGTACCTGTAAACATGGAATACCGGCCA-----AAAATAAGTTTGA 624
 QY 479 TATCATTTGAGAGATGGGCAATTTCCCTCATGGAATACCAAGTAACATTC 531
 479 TATCATTTGAGAGATGGGCAATTTCCCTCATGGAATACCAAGTAACATTC 531
 QY 625 TATCATTTGAGAGATGGGCAATTTCCCTCATGGAATACCAAGTAACATTC 677
 625 TATCATTTGAGAGATGGGCAATTTCCCTCATGGAATACCAAGTAACATTC 677

RESULT 12
 ABR84583
 ID ABR84583 standard; cDNA; 7260 BP.

AC ABR84583;

DT 14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #1154.

XX Human; ss: granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 CS Homo sapiens.
 PN WO200228999-A2.
 PN 11-APR-2002.
 PD 03-OCT-2001; 2001MO-US30821.
 PF 03-OCT-2000; 2000US-237189P.
 PR 03-OCT-2000; 2000US-237189P.
 XX
 XX (GENE-) GENE LOGIC INC.
 XX
 XX Beazer-Barclay Y, Weissman SM, Yamaga S., Vockley J.
 PI WPI; 2002-435328/46.
 XX
 DR Detecting granulocyte activation by detecting differential expression
 XX of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 XX
 PS Claim 1; SEQ ID No 1154; 114pp: English.
 XX
 XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection, and
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;
 Query Match 50.9%; Score 274.2; DB 24; Length 7260;

	Best Local Similarity	76.0%	Pred. No. 3,66-67;	
	Matches	405;	Conservative	0; Mismatches 68; Indels 60; Gaps 3
QY	1	GSACACAGAACCCCTTTCGGGGCTGAGCTGTGAGACCTCTTCAGTTGTTGTGACCA	60	
Db	311	GGACCCGGAAGACCTCTGGGGGGCTAGCTGTGATGCTCTTCAGTTCTGTGTGACAG	370	
QY	61	AGGGGCTTTACTTCAACAGAGCCCAAGCTATGAGCTCCACAGCAATGAGGAGGACACAG	120	
Db	371	AGGGGCTTTATTTATTAACAGAGCCCAAGGATGATGCTCCAGCAAGGAGGAGGCTTCAG	430	
QY	121	ACGGGCAATTGTGGATGAGTGTGTCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAC	180	
Db	431	ACAGGCACTGTGGATGAGTGTGTCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAT	490	
QY	181	TGTGTCCGTGCAAGCTTCAAAAGTCACTGTTCATCCGGGCCCAGGCCCACACTGAC	240	
Db	491	TGGGCAACCCCTCAACCTGTCCAGAGTCACTGTCTGTCCGTCCGCCACGCCCACCCGAC	550	
QY	241	ATGCCCAAGACTCAGAAAGTCCAGGCCCTATGCACACAAAGAAAGAGAGTGCAGAAAG	300	
Db	551	ATGCCCAAGACCCAG-----	565	
QY	301	ACAGGAAAGAGTATCACTTGAAGACACACAGTATGAGAGTGCAGAGAAACAGACCTTA	360	
Db	566	-----AAGGAGAGTACATTTGAAGAAAGCAAGTATGAGGAGTGCAGAGAAACAGACCTTA	618	
QY	361	CAGATGTAGAGAGAGCCCTCCGAGGAACAGAAATATGCCAGTCCACGAGATGCTTTG	420	
Db	619	CAGAGTGTAGAGAGAGCCCTCCGAGGAGTGAAGATGATCATGCCACCGCAGGATCCTTTG	678	
QY	421	-CTGCTGAGCAACCTGCCAAACACATGGAAACACCTGCCAAATATCATATATGATTCAA	478	
Db	679	CTGTGACAGAGTACTCTGTAACTTTGAGACACCTACCA-----AAAATATAGTTTGA	732	
QY	479	TATCATTTAGAGATGGGCATTTCCCTCAATGAATACACAACTAAACATTC	531	
Db	733	TATCATTTTAAAGATGGGCGTTTCCCCCAATGAATATCACAACTAAACATTC	785	
RESULT 13				
ABN97244				
ID	ABN97244	standard:	DNA;	7260 BP.
AC	ABN97244;			
XX				
DT	13-AUG-2002	(first entry)		
XX				
DE	Gene #3742	used to diagnose	Liver cancer.	
XX				
Gene:	Liver cancer;	ds;	hepatocellular carcinoma;	hepatocytotropic;
KW	metastatic liver tumour;	cytostatic;	expression profile;	disease state;
KM	disease progression;	drug toxicity;	drug efficacy;	drug metabolism.
XX				
OS	Homo sapiens.			
XX				
PN	MO200229103-A2.			
PD	11-APR-2002.			
XX				
PF	02-OCT-2001;	2001WO-US30589.		
XX				
PR	02-OCT-2000;	2000US-237054P.		
XX				
FA	(GENE-) GENE LOGIC INC.			
XX				
PI	Horne D, Alvaras C, Peres-Da-Silva S, Vockley JG;			
XX				
DR	WPI; 2002-426119/45.			
PT	Diagnosing and detecting the progression of liver cancer,			
PT	hepatocellular carcinoma or metastatic liver tumor in a patient,			
PT	involves detecting the level of expression of two or more genes in a			

PT Liver tissue sample -
XX
PS Claim 1, SEQ ID NO 3742; 298bp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytosolic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:
Query Match 50.9%; Score 274.2; DB 24; Length 7260;
Best Local Similarity 76.0%; Pred. No. 3.6e-67;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;
1 GGACCGAGAGACCCCTTGGGGGCTGAGCTGAGAGGCTTTCAGTTCGTGTGGACCA 60
311 GGACCGAGAGACCCCTTGGGGGCTGAGCTGAGAGGCTTTCAGTTCGTGTGGACCA 370
61 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGATTGGAGGCGCACACAG 120
371 AGGGGCTTTTATTTTAAACAAGCCCAAGGATGCTCCAGAGTGGAGGCGGCTCTGAG 430
121 ACGGGATTTGGATAGATGTTGCTTCCGAGCTGTGATCTGAGAGGCTGAGAGTAC 180
431 ACAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
181 TGTGTCCGCTGCAAGCTTACAAAGTACGCTCTTCATCCGCGGCGCCAGCCACTGAC 240
491 TGGGCAACCCCTCAAGCTGCGCAAGTACGCTGCTGTGCTGCTGCTGCTGCTGCTG 550
241 ATGCCCAAGCTCAGAGTCCCGAGCCCTTATGCACACACAAAGAAAGCTGCAAGG 300
551 ATGCCCAAGCTCAGAGTCCCGAGCCCTTATGCACACACAAAGAAAGCTGCAAGG 565
301 AGAAGCAAGAGTACACTTGAAGAACAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 360
566 -----AAGGAGTACATTGTAAGAAAGCAAGTGAAGAGTGAAGAGTGAAGAGTGAAG 618
361 CAGAAATGAGAGAGGCTCCGAGAGCAAGAAATGCCAGTCCAGCCGAGATCCTTTG 420
619 CAGAAATGAGAGAGGCTCCGAGAGCAAGAAATGCCAGTCCAGCCGAGATCCTTTG 478
421 --CTGGCTTGAAGCAAGCTGCAAAACATCGGAACACCTGCCAAATATCAATATAGTCA 478
679 CTCTGCGAGGATTAAGCTTTGAAGCTTTGAGACACCTTACCA-----AAAAATAGTTGA 732
479 TATCATTTAGAGATGGGCAATTTCCCTCAATGAATACAGCAAGTGAAGTTC 531
733 TACATTTAAAGATGGGCGTTTCCCGCAATGAATACAGCAAGTGAAGTTC 785
RESULT 14
ABK64812
ID ABK64812 standard; DNA; 7260 BP.
AC ABK64812;
XX
XX 18-JUN-2002 (first entry)
DT Human benign prostatic hyperplasia gene #707.
DE
XX

KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
XX Homo sapiens.
OS
XX MO200212440-A2.
PN
XX 14-FEB-2002.
PD
XX
XX 07-AUG-2001; 2001WO-US24708.
PF
XX 07-AUG-2000; 2000US-223323P.
PR
XX 05-JUN-2001; 2001US-0873319.
PX
XX (GENE-) GENE LOGIC INC.
PA
XX (NIBS) JAPAN TOBACCO INC.
PI
XX Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
DR WPI; 2002-257476/30.
XX
XX
XX PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
XX cells
XX
XX Disclosure; Page 391-393; 444pp; English.
XX
XX The invention relates to a method of diagnosing (I) the onset or
XX progression of benign prostatic hyperplasia (BPH), or screening (II) for
XX or identifying an agent that modulates the onset or progression of BPH.
XX The method is based on changes in gene expression in BPH tissue isolated
XX from patients exhibiting different clinical states of prostate
XX hyperplasia as compared to normal prostate tissue. (I) comprises
XX detecting the expression levels of one or more genes in prostate cells
XX from the subject that are differentially regulated compared to normal
XX prostate cells. (II) comprises preparing a first gene expression profile
XX of BPH cells or BPH-like cell population, exposing the cells to the
XX agent, preparing a second gene expression profile of the agent exposed
XX cells, and comparing the first and second gene expression profiles.
XX (I) is useful for diagnosing the onset or progression of BPH. (II) is
XX useful for identifying an agent that modulates the onset or progression
XX of BPH. The methods are useful to present information identifying
XX the expression level in a tissue or cells, by comparing the expression
XX level of genes given in the specification in the tissue or cells to the
XX level of expression of at least one gene in the database, and displaying the
XX expression levels of at least one gene in the tissue or cell sample
XX compared to the expression level in BPH. Agents using (II) are useful for
XX treating BPH or prostate cancer. ABK64106-ABK64860 represent human
XX benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:
Query Match 50.9%; Score 274.2; DB 24; Length 7260;
Best Local Similarity 76.0%; Pred. No. 3.6e-67;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;
1 GGACCGAGAGACCCCTTGGGGGCTGAGCTGAGAGGCTTTCAGTTCGTGTGGACCA 60
311 GGACCGAGAGACCCCTTGGGGGCTGAGCTGAGAGGCTTTCAGTTCGTGTGGACCA 370
61 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGATTGGAGGCGCACACAG 120
371 AGGGGCTTTTATTTTAAACAAGCCCAAGGATGCTCCAGAGTGGAGGCGGCTCTGAG 430
121 ACGGGATTTGGATAGATGTTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGAC 180
431 ACAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
181 TGTGTCCGCTGCAAGCTTACAAAGTACGCTCTTCATCCGCGGCGCCAGCCACTGAC 240
491 TGGGCAACCCCTCAAGCTGCGCAAGTACGCTGCTGTGCTGCTGCTGCTGCTGCTG 550
241 ATGCCCAAGCTCAGAGTCCCGAGCCCTTATGCACACACAAAGAAAGCTGCAAGG 300

DB 551 ATGCCCAAGACCCAG----- 565
QY 301 AGAAGAAAAGAGTACTTGAGACACAAAGTAGAGAGTGCAGGAAACAGACCTA 360
DB 566 -----AAGGAAAGTACATTGTAAGACCAAGTAGAGAGAGTGCAGGAAACAGACTA 618
QY 361 CAGATGTAGAGAGAGCTCCCGAGAGACAGAAATGCGACAGTCCAGATCCTTG 420
DB 619 CAGAGTGTAGAGAGACCTCTCCGAGAGTGAAGAGTGCACAGCCGAGAGTCTTG 678
QY 421 --CTGCTTGAGCACTCCAAACATCGAACACCTGCCAATATCATTAATGATTCAA 478
DB 679 CTCTGACAGAGTTACCTGTTAACTTGTGAACACCTACCA-----AAAAATAGTTGA 732
QY 479 TATCATTTAGAGATGGGATTTCCCTCAATGAATATACAAAGTAAATTC 531
DB 733 TACATTTTAAAGATGGGCTTCCCAATGAATACAAAGTAAACATTCC 785
RESULT 15
ABK35504
ID ABK35504 standard; DNA; 7260 BP.
XX
AC ABK35504;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human endometrial cancer related gene, IGFL.
XX
KM Human; ds; gene; endometrial cancer; differential expression;
KM DNA microarray; protein microarray.
XX
OS Homo sapiens.
XX
PN WO200209573-A2.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US24104.
XX
PR 31-JUL-2000; 2000US-221735P.
XX
PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Mutter GL;
XX
DR WPI: 2002-179967/23.
DR P-PSDB: AAUB4284.
XX
PT Diagnosing endometrial cancer comprises determining expression of
PT nucleic acid molecules or expression products that are differentially
PT expressed in normal and malignant endometrium -
XX
PS Claim 1; Page 85-89; 233pp; English.
XX
CC The invention relates to diagnosing endometrial cancer in a subject
CC suspected of having endometrial cancer comprising determining the
CC expression of a set of nucleic acid molecules or expression products in
CC an endometrial sample suspected of being cancerous, where the set of
CC nucleic acid molecules comprises at least 2 nucleic acid molecules
CC selected from 50 fully defined sequences as given in the specification.
CC The nucleic acids are used as an array of at least 2 of the 50
CC nucleic acids bound to a solid substrate. Also included is a solid-phase
CC protein microarray comprising at least 2 antibodies or its antigen
CC binding fragments, that specifically bind at least 2 different
CC polypeptides from the 50 fully defined sequences as given in the
CC specification, fixed to a solid substrate. The methods and arrays are
CC useful for the diagnosis of endometrial cancer, selecting and monitoring
CC treatment regimes and identification of lead compounds useful for the
CC treatment of endometrial cancer. The present sequence is one of 50
CC genes differentially expressed between cancerous and non-cancerous
CC samples.

XX Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;
SQ
Query Match 50.9%; Score 274.2; DB 24; Length 7260;
Best Local Similarity 76.0%; Pred. No. 3,6e-67;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;
QY 1 GGACCAAGACCCCTTTCGGGGCTGAGCTGTGTGAGAGCTTTCAGTTCTGTGTGACCA 60
DB 311 GGACGGAGAGAGCTCTCCGGGGCTGAGCTGTGTGAGAGCTTTCAGTTCTGTGTGAGAG 370
QY 61 AGGGGCTTTACTTCAACAAGCCCAAGTATAGCTCCAGATTCGAGGGGACACAG 120
DB 371 AGGGGCTTTATTTCACAAGCCCAAGSTATAGCTCCAGCTGTGGAGGGGCTCAG 430
QY 121 ACGGCACTTGATGATGATGTTCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
DB 431 ACAGGCATCGTGTGATGATGTTCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAT 490
QY 181 TGTGCTCGCTGCAAGCCTACAAAGTCAAGTCACTGCTTCATCGGGGCGCCAGCACTGAC 240
DB 491 TCGGCACCCCTCAAGCTGCAAGTCAAGTCACTGCTTCGTTCCGTCGCCAGCGCCACACGAC 550
QY 241 ATGCCCAAGACTCAGAAAGTCCAGCCCTATCGACACACAGAAAAGAAAGTGCAGAGG 300
DB 551 ATGCCCAAGACCCAG----- 565
QY 301 AGAAGAAAAGAGTACTTGAGACACAAAGTACAGAGTGCAGAGAAACAGACCTA 360
DB 566 -----AAGGAAAGTACATTGTAAGACCAAGTAGAGAGTGCAGGAAACAGACTA 618
QY 361 CAGATGTAGAGAGAGCTCCCGAGAGACAGAAATGCGACAGTCCAGATCCTTG 420
DB 619 CAGAGTGTAGAGAGACCTCTCCGAGAGTGAAGAGTGCACAGCCGAGAGTCTTG 678
QY 421 --CTGCTTGAGCACTCCAAACATCGAACACCTGCCAATATCATTAATGATTCAA 478
DB 679 CTCTGACAGAGTTACCTGTTAACTTGTGAACACCTACCA-----AAAAATAGTTGA 732
QY 479 TATCATTTAGAGATGGGATTTCCCTCAATGAATATACAAAGTAAATTC 531
DB 733 TACATTTTAAAGATGGGCTTCCCAATGAATACAAAGTAAACATTCC 785

Search completed: June 15, 2003, 16:08:49
Job time : 165.509 secs

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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:46:38 ; Search time 43.6935 Seconds
(without alignments)
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Title: US-09-852-261-3

Perfect score: 539

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Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/prodata/2/ina/fa_COMB.seq:*
3: /cgn2_6/prodata/2/ina/fa_COMB.seq:*
4: /cgn2_6/prodata/2/ina/fa_COMB.seq:*
5: /cgn2_6/prodata/2/ina/fa_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356.8	66.2	553	4	US-09-142-583A-3
2	356.8	66.2	553	4	US-09-142-583A-5
3	272.6	50.6	777	4	US-09-142-583A-10
4	271	50.3	622	6	5405942-2
5	222	41.2	5707	2	US-08-472-809F-8
6	222	41.2	6345	2	US-08-472-809F-7
7	205.2	38.1	357	6	5405942-9
8	203.6	37.8	337	6	5405942-13
9	166.8	30.9	210	6	5405942-7
10	166.8	30.9	210	6	5405942-11
11	166.8	30.9	2862	4	US-09-255-829-13
12	165.2	30.6	210	6	5405942-15
13	161.2	29.9	240	1	US-08-308-196A-1
14	161.2	29.9	240	5	PCT-US81-06452-1
15	161.2	29.9	350	3	US-09-029-267-13
16	151.4	28.8	798	1	US-07-953-230A-6
17	146	27.1	770	1	US-07-953-230A-1
18	146	27.1	846	1	US-07-953-230A-5
19	118.6	22.0	621	3	US-08-989-251-40
20	118.6	22.0	621	3	US-09-340-250-40
21	118.6	22.0	621	4	US-09-528-108-40
22	110.8	20.4	243	2	US-08-82-182-75
23	109.8	20.4	485	1	US-07-989-845-29
24	109.8	20.4	485	1	US-07-989-844-13
25	109.8	20.4	485	1	US-08-110-663-11
26	109.8	20.4	485	1	US-08-169-688-11
27	109.8	20.4	485	1	US-08-240-121-13

28	109.8	20.4	485	1	US-08-451-241-13	Sequence 13, Appl
29	109.8	20.4	485	1	US-08-110-664-1	Sequence 1, Appl
30	109.8	20.4	485	1	US-08-446-882-1	Sequence 1, Appl
31	109.8	20.4	485	1	US-08-385-187A-1	Sequence 1, Appl
32	109.8	20.4	485	1	US-08-470-108-1	Sequence 1, Appl
33	109.8	20.4	485	5	PCT-US93-11297-13	Sequence 13, Appl
34	109.8	20.4	485	5	PCT-US93-11298-29	Sequence 29, Appl
35	109.2	20.3	237	1	US-07-764-655D-8	Sequence 9, Appl
36	107.6	20.0	717	1	US-08-284-784-40	Sequence 40, Appl
37	107.6	20.0	717	1	US-08-284-784-40	Sequence 40, Appl
38	107.6	20.0	783	2	US-08-854-811-43	Sequence 43, Appl
39	107.6	20.0	783	2	US-08-854-811-43	Sequence 43, Appl
40	107.6	20.0	891	1	US-08-284-784-33	Sequence 33, Appl
41	107.6	20.0	891	1	US-08-284-784-33	Sequence 33, Appl
42	107.6	20.0	891	1	US-08-854-811-33	Sequence 33, Appl
43	107.6	20.0	891	2	US-08-854-811-34	Sequence 34, Appl
44	107.6	20.0	900	1	US-08-284-784-24	Sequence 24, Appl
45	107.6	20.0	900	1	US-08-284-784-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-142-583A-3
Sequence 3, Appl
Patent No. 6221942

GENERAL INFORMATION:

APPLICANT: GOLDSPIK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA

NAME/KEY: CDS
LOCATION: 1..363
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3

Query Match 66.2%, Score 356.8; DB 4; Length 553;

Best Local Similarity 82.3%; Pred. No. 1.9e-109;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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DB 31 GGACCGAGAGAGCTCTGGGGTGTGAGCTGTGAGCTCTTCTGCTGTGTGAGAC 90
QY 61 AGGGGCTTTTACTTCAACAGCCACAGTATGCTCCAGCATTCGAGGGGACCCAG 120
DB 91 AGGGGCTTTTATTTCACAGCCACAGATAGGGCTCCAGCATTCGAGGGGACCCAG 150
QY 121 ACGGCACTTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAC 180
DB 151 ACGGCACTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAC 210
QY 181 TGTGCTCGCTCAAGCCCTACAAAGCTGCTGCTCCATCCGAGGGCCGACCCACACTGAC 240
DB 211 TGTGACACCCCTCAAGCCGCGCAAGGACCCGCTCCGCTGCTGCGGACCCGACCCGAC 270
QY 241 ATGCCCAAGACTCAGAAAGTCCCGAGCCCTATCGACACAGAAAGAAAGCTGCAAAAG 300
DB 271 ATGCCCAAGACTCAGAAAGTATCAGCTCTCATCTCCACAAAGAAAGTCAAGTCTCAGAG 330
QY 301 AGAAGAAAGAAAGTAACTGAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 331 AGAAGAAAGAAAGTAACTGAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 390
QY 361 CAGAAATGAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 391 CAGAAATGAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
QY 421 CTGCTTGAAGACCTGCAAAACATCGAAGACAGCTGCAAAATATCAATATGAGTTCATA 480
DB 451 CTGCTGACACTTACTCTTAACATGGAATGAGATCCGGCCCA-----AAAAATGATTGATC 504
QY 481 TCATTTGAGAGATGGGCAATTCCTCATGTAATATACAGAGTAACATTC 530
DB 505 ACATTTCAAGAT-GGCATTTCCCGCAATGAAATATACAGAGTAACATTC 553
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RESULT 2

US-09-142-583A-5
Sequence 5, Application US/09142583A
Patent No. 6221842
GENERAL INFORMATION:
APPLICANT: GOLDSPIK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 341..397

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 66.2%; Score 356.8; DB 4; Length 553;
Best Local Similarity 82.3%; Pred. No. 1.9e-109;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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QY 1 GGACGAGAGACCCCTTTGGGGGGCTGAGCTGTGAGACCTCTTCTGCTGTGTGAGACCA 60
DB 31 GGACCGAGAGAGCTCTGGGGTGTGAGCTGTGAGCTCTTCTGCTGTGTGAGAC 90
QY 61 AGGGGCTTTTACTTCAACAGCCACAGTATGCTCCAGCATTCGAGGGGACCCAG 120
DB 91 AGGGGCTTTTATTTCACAGCCACAGATAGGGCTCCAGCATTCGAGGGGACCCAG 150
QY 121 ACGGCACTTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAC 180
DB 151 ACGGCACTGTGATGAGTGTGCTTCCGAGCTGTATCTGAGAGGCTGAGATGTAC 210
QY 181 TGTGCTCGCTCAAGCCCTACAAAGCTGCTGCTCCATCCGAGGGCCGACCCACACTGAC 240
DB 211 TGTGACACCCCTCAAGCCGCGCAAGGACCCGCTCCGCTGCTGCGGACCCGACCCGAC 270
QY 241 ATGCCCAAGACTCAGAAAGTCCCGAGCCCTATCGACACAGAAAGAAAGCTGCAAAAG 300
DB 271 ATGCCCAAGACTCAGAAAGTATCAGCTCTCATCTCCACAAAGAAAGTCAAGTCTCAGAG 330
QY 301 AGAAGAAAGAAAGTAACTGAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 331 AGAAGAAAGAAAGTAACTGAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 390
QY 361 CAGAAATGAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 391 CAGAAATGAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
QY 421 CTGCTTGAAGACCTGCAAAACATCGAAGACAGCTGCAAAATATCAATATGAGTTCATA 480
DB 451 CTGCTGACACTTACTCTTAACATGGAATGAGATCCGGCCCA-----AAAAATGATTGATC 504
QY 481 TCATTTGAGAGATGGGCAATTCCTCATGTAATATACAGAGTAACATTC 530
DB 505 ACATTTCAAGAT-GGCATTTCCCGCAATGAAATATACAGAGTAACATTC 553
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RESULT 3

US-09-142-583A-10
Sequence 10, Application US/09142583A
Patent No. 6221842
GENERAL INFORMATION:
APPLICANT: GOLDSPIK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:

RESULT 6
US-08-472-809B-7

QY	1	GGACGAGAACCCCTTTGGGGGGCTAGCTGGTGGAGCCCTTCAGTTTCGTGTGGACCA	60
Db	3702	GGACCGGAGAACCCCTTCGGGGGGCTAGCTGGTGGATCTCTTACGTTTCGTGTGGACAC	3765
QY	61	AGGGGCTTTTACTTCACAGACCCACAGTATGCTTCACGATTCGGAGGGCACCCACAG	120
Db	3762	AGGGGCTTTTATTTTCAACAGACCCACAGGGATATGCTTCACGAGTGGAGAGGGCCCTCAG	3822
QY	121	ACGGGCTATTGGAGATGAGTGTTCCTTCCGAGAGCTGTATCTGAGAGAGCTGGAGATGTAC	180
Db	3822	ACAGGGATCTGGATGATGATGTCTGCTCCCGAGAGCTGTATCTTAAAGGAGGCTGGAGATGTAT	3885
QY	181	TGTGTCCGCTGCAAGCCCTACAAAGTCAGCTGTTCATCCGGGCCCCAGGCCACACTGAC	240
Db	3882	TGCGCACCCCTCAAGCCTGCACAGTCAGCTGTCTGTCCGTGCCACAGGCCACACAGCAC	3942
QY	241	ATGCCCAAGACTCGAGAACTCCAGCCCCCTATCGACACACAGAAAAGGAAAGCTGCAGAGG	300
Db	3942	ATGCCCAAGACCCCA-----	3955

APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO: 11
LENGTH: 210
5405942-11

Query Match
Best Local Similarity 30.9%; Score 166.8; DB 6; Length 210;
Matches 183; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTTGCGGGGCTGAGCTGTGAGAGCTTTCAGTTGCTGTGAGACCA 60
DB 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGTGAGAGCTTTCAGTTGCTGTGAGAG 60
QY 61 AGGGGCTTTTACTTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACACAG 120
DB 61 AGGGGCTTTTATTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACACAG 120
QY 121 ACGGGCATTTGTGATGATGATGCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGAT 180
DB 121 ACGAGTATCGTGTGATGATGCTCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGAT 180
QY 181 TGTGTCGCTGCAAGCTTACCAAGTCAGCT 210
DB 181 TGGCGACCCCTCAAGCCTGCGCAAGTCAGCT 210

RESULT 11
US-09-255-829-13
Sequence 13, Application US/09255829
Patent No. 6461617

GENERAL INFORMATION:

APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Pedralig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPC)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/255,829

FILING DATE: 23-FEB-1999

Prior Application DATA:

APPLICATION NUMBER: PCT/GB97/02273

FILING DATE: 22-AUG-1997

Prior Application DATA:

APPLICATION NUMBER: US 08/782,893

FILING DATE: 27-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1581.0130002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 2862 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS
LOCATION: 1..2862
US-09-255-829-13

Query Match
Best Local Similarity 30.9%; Score 166.8; DB 4; Length 2862;
Matches 183; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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DB 2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGTGAGAGCTTTCAGTTGCTGTGAGAG 2703
QY 61 AGGGGCTTTTACTTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACACAG 120
DB 2704 AGGGGCTTTTATTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACACAG 120
QY 121 ACGGGCATTTGTGATGATGATGCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGAT 180
DB 2764 ACGAGTATCGTGTGATGATGCTCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGAT 180
QY 181 TGTGTCGCTGCAAGCTTACCAAGTCAGCT 210
DB 2824 TGGCGACCCCTCAAGCCTGCGCAAGTCAGCT 2853

RESULT 12
5405942-15
Patent No. 5405942

APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER, JAMES P.

TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

I AND II

NUMBER OF SEQUENCES: 16

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/65,673

FILING DATE: 16-JUN-1987

Prior Application DATA:

APPLICATION NUMBER: 630,557

FILING DATE: 19-JUL-1984

SEQ ID NO: 15

LENGTH: 210

5405942-15

Query Match
Best Local Similarity 30.6%; Score 165.2; DB 6; Length 210;
Matches 141; Conservative 41; Mismatches 28; Indels 0; Gaps 0;

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DB 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGTGAGAGCTTTCAGTTGCTGTGAGAG 60
QY 61 AGGGGCTTTTACTTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACACAG 120
DB 61 AGGGGCTTTTATTCAACAGCCCAAGCTATGCTCCAGCATTTGGAGAGCCACACAG 120
QY 121 ACGGGCATTTGTGATGATGATGCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGAT 180
DB 121 ACGAGTATCGTGTGATGATGCTCTTCCGAGAGCTGTGATCTGAGAGAGCTGAGATGAT 180
QY 181 TGTGTCGCTGCAAGCTTACCAAGTCAGCT 210
DB 181 TGGCGACCCCTCAAGCCTGCGCAAGTCAGCT 210

RESULT 13
US-08-308-196A-1
Sequence 1, Application US/08308196A

Patent No. 5612198

GENERAL INFORMATION:

APPLICANT: Briertley, Russell A.

APPLICANT: Davis, Geneva R.

APPLICANT: Holtz, Gregory C.

APPLICANT: Gleeson, Martin A.

```

1  APPLICANT: Bradley, D. H.
2  TITLE OF INVENTION: Production of Insulin-Like Growth
3  TITLE OF INVENTION: Factor-I in Methylophilic Yeast Cells
4  NUMBER OF SEQUENCES: 12
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Fitch, Even, Tabin & Flannery
7  STREET: 135 South Lasalle Street, Suite 900
8  CITY: Chicago
9  STATE: Illinois
10 COUNTRY: USA
11 ZIP: 60603
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: PCT/US91/06452
20 FILING DATE: 19910409
21 CLASSIFICATION: 435
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/578,728
24 FILING DATE: 04-SEP-1990
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Seidman, Stephanie L.
27 REGISTRATION NUMBER: 33,779
28 REFERENCE/DOCKET NUMBER: 51874
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (619)552-1311
31 TELEFAX: (619)552-0095
32 INFORMATION FOR SEQ. ID NO.: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 240 base pairs
35 TYPE: NUCLEIC ACID
36 STRANDEDNESS: double
37 TOPOLOGY: unknown
38 MOLECULE TYPE: CDNA
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: 14..232
42 PCT-US91-06452-1
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44 Query Match 29.9%; Score 161.2; DB 5; Length 240;
45 Best Local Similarity 84.6%; Pred. No. 2.6e-44;
46 Matches 181; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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49 Db 17 GCACCGAAGACCCCTTGCGGGCTAGCTGGTGGACGCGCTTCAGTTCGTGTGGAC 76
50 QY 61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGAGCTCCACATTCCGAGGGCACACAG 120
51 Db 77 AGGGGCTTTTATTTCACAAGCCACAGCGATATGAGCTCCACAGTCCAGCGGCGCTCAG 136
52 QY 121 ACGGGATTTGTGGAGAGCTGTGCTTCGGGAGCTGTATCTGAGAGAGGCTGGAGATTAC 180
53 Db 137 ACGAGCTTTGTGGATGAGAGCTGTGCTTCGGGAGCTGTATCTTAAGAGAGCTTCAGATTAT 196
54 QY 181 TGTGTCGGTCCAGACCTACAAGAGTCAAGTCTGTT 214
55 Db 197 TCGGACCCCTCAAGCTTCGCCAAGTCAGCTTGAT 230
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57 RESULT 15
58 US-09-029-267-13
59 Sequence 13, Application US/09029267
60 Patent No. 6107057
61 GENERAL INFORMATION:
62 APPLICANT: Crawford, Kenneth
63 APPLICANT: Zarot, Isabel
64 APPLICANT: Innis, Michael
65 TITLE OF INVENTION: Pichia Secretary Leader for Protein
66 TITLE OF INVENTION: Expression

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NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: United States
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,267
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 1165.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2704
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-09-029-267-13

Query Match 29.98; Score 161.2; DB 3; Length 390;
Best Local Similarity 84.6%; Pred. No. 3.4e-44;
Matches 181; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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DB 160 GGACCGAGAGAGCTGCGGGGGCTGAGCTGTGATGCTGTGCTGTGTGTGAGAC 219
QY 61 AGGGGCTTTACTTCACACAGCCACAGTCTATGCTCCAGCATTCGAGAGGACACACAG 120
DB 220 AGGGGCTTTATTTCACACAGCCACAGGATAGGCTCCAGCATTCGAGAGGAGGCTCAG 279
QY 121 ACGGCGATTGTGATGATGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180
DB 280 ACGGCGATGCTGATGATGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAT 339
QY 181 TGTGTCCGTGCAAGCTACAAAGTCACTCTT 214
DB 340 TGGCGACCCCTCAAGCCTGCCAAGTCACTGTAT 373

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Job time : 44.6935 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 17:22:19 ; Search time 97.6276 Seconds

(Without alignments)
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Title: US-09-852-261-3

Perfect score: 539

Sequence: 1 ggaccagagacccttgagg.....agtaaacattcccggaattc 539

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	425	78.8	487 10 US-09-852-261-11	Sequence 11, Appl1
4	356.8	66.2	523 10 US-09-852-261-5	Sequence 5, Appl1
5	325.2	60.3	517 10 US-09-852-261-1	Sequence 1, Appl1
6	274.2	50.9	7260 9 US-10-136-639-4	Sequence 4, Appl1
7	274.2	50.9	10 US-09-919-497-24	Sequence 24, Appl1
8	274.2	50.9	7260 10 US-09-880-107-3739	Sequence 3739, Ap
9	262	48.6	471 10 US-09-852-261-13	Sequence 13, Appl1
10	213.8	39.7	286 9 US-10-161-088-3	Sequence 3, Appl1
11	205.8	38.4	318 10 US-09-852-261-9	Sequence 9, Appl1
12	205.6	37.8	462 9 US-10-238-114-1	Sequence 1, Appl1
13	164.6	30.5	4532 10 US-09-930-377B-1	Sequence 1, Appl1
14	163.6	30.4	210 10 US-09-930-377B-2	Sequence 2, Appl1
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18	118.6	22.0	621 9 US-10-280-826-40	Sequence 40, Appl1
19	118.6	22.0	621 10 US-09-921-398-40	Sequence 40, Appl1

20	105.4	19.6	480 9 US-10-280-826-38	Sequence 38, Appl1
21	105.4	19.6	480 10 US-09-921-398-38	Sequence 38, Appl1
22	67.4	12.5	411 10 US-09-960-352-2082	Sequence 2082, Ap
23	67.2	12.5	437 9 US-10-066-543-663	Sequence 663, App
24	67.2	12.5	493 9 US-10-066-543-997	Sequence 997, App
25	67.2	12.5	518 9 US-10-066-543-1040	Sequence 1040, Ap
26	67.2	12.5	536 9 US-10-066-543-428	Sequence 428, App
27	67.2	12.5	543 9 US-10-136-841-1	Sequence 1, Appl1
28	67.2	12.5	549 9 US-10-066-543-478	Sequence 478, App
29	67.2	12.5	574 9 US-10-025-380-918	Sequence 918, App
30	67.2	12.5	574 10 US-09-922-217-918	Sequence 918, App
31	67.2	12.5	574 10 US-09-833-263-918	Sequence 918, App
32	67.2	12.5	577 9 US-10-066-543-1137	Sequence 1137, Ap
33	67.2	12.5	579 9 US-10-066-543-1034	Sequence 1034, Ap
34	67.2	12.5	586 9 US-10-066-543-808	Sequence 808, App
35	67.2	12.5	1356 9 US-10-081-119-37	Sequence 37, Appl1
36	67.2	12.5	1356 9 US-10-097-340-144	Sequence 144, App
37	67.2	12.5	1356 10 US-09-962-436-293	Sequence 293, App
38	67.2	12.5	1356 10 US-09-954-456-294	Sequence 294, App
39	67.2	12.5	1356 10 US-09-880-107-2092	Sequence 2092, Ap
40	67.2	12.5	4350 9 US-10-123-181-37	Sequence 37, Appl1
41	66	12.2	854 9 US-09-954-531-989	Sequence 989, App
42	65.8	12.2	447 9 US-10-025-380-917	Sequence 917, App
43	65.8	12.2	447 10 US-09-922-217-917	Sequence 917, App
44	65.8	12.2	447 10 US-09-833-263-917	Sequence 917, App
45	62.4	11.6	237 9 US-10-136-841-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1				
US-09-852-261-3				
Sequence 3, Appl1 Application US/09852261				
Patient No. US20020083477A1				
GENERAL INFORMATION:				
APPLICANT: GOLDSPIRK, GEOFFREY				
APPLICANT: TERENCE, GIORGIO				
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE				
FILE REFERENCE: 117-351				
CURRENT APPLICATION NUMBER: US/09/852,261				
CURRENT FILING DATE: 2001-05-10				
PRIOR APPLICATION NUMBER: GB 0011278.9				
PRIOR FILING DATE: 2000-05-10				
NUMBER OF SEQ ID NOS: 14				
SOFTWARE: PatentIn Ver. 2.1				
SEQ ID NO 3				
LENGTH: 539				
ORGANISM: Rattus sp.				
US-09-852-261-3				
Query Match				
Best Local Similarity 100.0%; Pred No. 3.9e-171;				
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	GGACCAAGAGACCTTTCGCGGGCTGAGCTGTGAGACGCTTTCAGTTCGTGTGTGACCA	60	
DB	1	GGACCAAGAGACCTTTCGCGGGCTGAGCTGTGAGACGCTTTCAGTTCGTGTGTGACCA	60	
QY	61	AGGGGCTTTCCTACACAGCCCAAGCTATGCTCCAGATTCGAGGGCCACACAG	120	
DB	61	AGGGGCTTTCCTACACAGCCCAAGCTATGCTCCAGATTCGAGGGCCACACAG	120	
QY	121	ACGGGATTTGATGATGATGCTTCCGAGCTGATGATGAGAGGCTGAGATGATC	180	
DB	121	ACGGGATTTGATGATGATGCTTCCGAGCTGATGATGAGAGGCTGAGATGATC	180	
QY	181	TGTGTCCGTGCAAGCTTCAAAAGTCAAGTCTGTTCCATCCGGGCCACGCACTGAC	240	
DB	181	TGTGTCCGTGCAAGCTTCAAAAGTCAAGTCTGTTCCATCCGGGCCACGCACTGAC	240	
QY	241	ATGCCCAAGACACAGAGTCCAGCCCTTATGACACACAAAGAGAGTGAAGG	300	

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Db 241 ATGCCAAGACTCAGAGTCCACGCCCTATGACACACAGAAAGAGGTGCAAGG 300
Oy 301 AGAAGAAAGAGAGTACACTTGAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 360
Db 301 AGAAGAAAGAGAGTACACTTGAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 360
Oy 361 CAGAAATGTAGAGAGGAGGCTCCCGAGAGACAGAAATGCCAGCTCACCGCAAGATCCTTG 420
Db 361 CAGAAATGTAGAGAGGAGGCTCCCGAGAGACAGAAATGCCAGCTCACCGCAAGATCCTTG 420
Oy 421 CTGCTTGACCAACTGCAAAACATCGAAGACCTGCCAAATATCAATATAGTTCATA 480
Db 421 CTGCTTGACCAACTGCAAAACATCGAAGACCTGCCAAATATCAATATAGTTCATA 480
Oy 481 TCATTTCAGAGATGGGCAATTTCCCTCATGAATACACAGAAACATTTCCCGAATTC 539
Db 481 TCATTTCAGAGATGGGCAATTTCCCTCATGAATACACAGAAACATTTCCCGAATTC 539
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RESULT 2

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US-10-161-088-1
; Sequence 1, Application US/10161088
; Publication No. US2003007761A1
; GENERAL INFORMATION:
; APPLICANT: Parrow, Vendela
; APPLICANT: Rosegren, Linda
; TITLE OF INVENTION: NEW METHODS
; FILE REFERENCE: 13425-111001
; CURRENT APPLICATION NUMBER: US/10/161,088
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(471)
US-10-161-088-1
```

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Query Match 84.2%; Score 453.8; DB 9; Length 651;
Best Local Similarity 92.8%; Pred. No. 2.2e-142;
Matches 476; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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Oy 1 GGACAGAGAGACCTTTGCGGGGCTGAGTGGTGAAGCTTCAATGCTGTGTGACCA 60
Db 139 GAGCCAGAGAGACCTTTGCGGGGCTGAGTGGTGAAGCTTCAATGCTGTGTGACCG 198
Oy 61 AGGGGCTTTTACTTCAACAGCCACAGTCTATGGCTCCAGCATTCGAGGGCACCACAG 120
Db 199 AGGGGCTTTTACTTCAACAGCCACAGGCTATGGCTCCAGCATTCGAGGGCACCACCTAG 258
Oy 121 ACGGGCATTTGTGATGAGTGTGCTCCGAGCTGTGATCTGAGAGGTGAGATGTAC 180
Db 259 ACGGGCATTTGTGATGAGTGTGCTCCGAGCTGTGATCTGAGAGGTGAGATGTAC 318
Oy 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGTCTGCTTCATCTCCGAGCCAGCCACACTGAC 240
Db 319 TGTGTCGCTGCAAGCTTCAAAAGTCAAGGCGGCTCTATCTCGCCAGGCCACACTGAC 378
Oy 241 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGACACACAGAAAGAGAGTGCAGAGG 300
Db 379 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGACAAACAAAGAAACAGAGTGCAGAGG 438
Oy 301 AGAAGAAAGAGAGTACACTTGAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 360
Db 439 AGAAGAAAGAGAGTACACTTGAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 498
Oy 361 CAGAAATGTAGAGAGGCTCCCGAGAGACAGAAATGCCAGCTCACCGCAAGATCCTTG 420
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Db 499 CAGAAATGTAGAGAGGCTCCAGCGAGACAGAAATGCCAAATATCAATATAGTTCATA 558
Oy 421 CTGCTTGACCAACTGCAAAACATCGAAGACCTGCCAAATATCAATATAGTTCATA 480
Db 559 CTGCTTGACCAACTGCAAAACATCGAAGACCTGCCAAATATCAATATAGTTCATA 618
Oy 481 TCATTTCAGAGATGGGCAATTTCCCTCATGAATA 513
Db 619 ACATTACAAAGATGGGCAATTTCCCGCAATGAAA 651
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RESULT 3

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US-09-852-261-11
; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-11
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Query Match 78.8%; Score 425; DB 10; Length 487;
Best Local Similarity 90.4%; Pred. No. 9.4e-133;
Matches 487; Conservative 0; Mismatches 0; Indels 52; Gaps 1;
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Oy 1 GGACAGAGAGACCTTTTGGGGGCTGAGTGGTGAAGCTTCAATGCTGTGTGACCA 60
Db 1 GGACAGAGAGACCTTTTGGGGGCTGAGTGGTGAAGCTTCAATGCTGTGTGACCA 60
Oy 61 AGGGGCTTTTACTTCAACAGCCACAGTCTATGGCTCCAGCATTCGAGGGCACCACAG 120
Db 61 AGGGGCTTTTACTTCAACAGCCACAGTCTATGGCTCCAGCATTCGAGGGCACCACAG 120
Oy 121 ACGGGCATTTGTGATGAGTGTGCTCCGAGCTGTGATCTGAGAGGTGAGATGTAC 180
Db 121 ACGGGCATTTGTGATGAGTGTGCTCCGAGCTGTGATCTGAGAGGTGAGATGTAC 180
Oy 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGTCTGCTTCATCTCCGAGCCAGCCACACTGAC 240
Db 181 TGTGTCGCTGCAAGCTTCAAAAGTCAAGTCTGCTTCATCTCCGAGCCAGCCACACTGAC 240
Oy 241 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGACACACAGAAAGAGAGTGCAGAGG 300
Db 241 ATGCCCAAGACTCAGAGAGTCCAGCCCTATGACACACAGAAAGAGAGTGCAGAGG 300
Oy 301 AGAAGAAAGAGAGTACACTTGAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 360
Db 301 AGAAGAAAGAGAGTACACTTGAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 360
Oy 361 CAGAAATGTAGAGAGGCTCCCGAGAGACAGAAATGCCAGCTCACCGCAAGATCCTTG 420
Db 361 CAGAAATGTAGAGAGGCTCCCGAGAGACAGAAATGCCAGCTCACCGCAAGATCCTTG 420
Oy 421 CTGCTTGACCAACTGCAAAACATCGAAGACCTGCCAAATATCAATATAGTTCATA 480
Db 421 CTGCTTGACCAACTGCAAAACATCGAAGACCTGCCAAATATCAATATAGTTCATA 480
Oy 481 TCATTTCAGAGATGGGCAATTTCCCTCATGAATA 513
Db 481 TCATTTCAGAGATGGGCAATTTCCCTCATGAATA 513
Oy 429 TCATTTCAGAGATGGGCAATTTCCCTCATGAATA 487
Db 429 TCATTTCAGAGATGGGCAATTTCCCTCATGAATA 487
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RESULT 4
US-09-852-261-5
Sequence 5, Application US/09852261
Patent No. US20020083477A1
GENERAL INFORMATION:
APPLICANT: GOLDSPIRK, GEOFFREY
APPLICANT: TERENCE, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
FILE REFERENCE: 117-351
CURRENT APPLICATION NUMBER: US/09/852,261
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GB 0011278.9
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 5
LENGTH: 523
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
US-09-852-261-5

Query Match 66.2%; Score 356.8; DB 10; Length 523;
Best Local Similarity 82.3%; Pred. No. 9.4e-110;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;
QY 1 GGACCCAGAGACCCCTTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGACCA 60
Db 1 GGACCCAGAGAGCTCTCGGGTGTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGAG 60
QY 61 AGGGGCTTTTACTTCAACAGCCGACAGCTATGCTCCAGCATTCGAGAGGCAACACAG 120
Db 61 AGGGGCTTTTATTCAACAGCCGACAGCTATGCTCCAGCATTCGAGAGGCAACCTCAG 120
QY 121 ACAGGCACTGTGATGATGATGCTTCCGAGCTGTGATGATGATGATGATGATGATGAT 180
Db 121 ACAGGCACTGTGATGATGATGCTTCCGAGCTGTGATGATGATGATGATGATGATGAT 180
QY 181 TGATGCTGCTGCAAGCTTCAACAGCTGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 TGATGCTGCTGCAAGCTTCAACAGCTGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATGCCCAAGACTCGAAGTCCGAGCCCTATCCGACACAGAAAGAGAGCTGCAAGG 300
Db 241 ATGCCCAAGACTCGAAGTCCGAGCCCTATCCGACACAGAAAGAGAGCTGCAAGG 300
QY 301 AGAAGGAAGAGAGTACACTTGAAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AGAAGGAAGAGAGTACACTTGAAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CAGAGTGTAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 CAGAGTGTAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 CTGCTTGAAGACCTGCAAAACATCGAAGACCTGCAAAATATCAATATGATGATGATGAT 480
Db 421 CTGCTGACAGTGTACCTGATTAACATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 TCATTTAG 540
Db 481 TCATTTAG 540
QY 541 ACATTTCAAGAGT-GGCAATTTCCCGCAATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 ACATTTCAAGAGT-GGCAATTTCCCGCAATGATGATGATGATGATGATGATGATGATGAT 600

RESULT 5
US-09-852-261-1
Sequence 1, Application US/09852261
Patent No. US20020083477A1
GENERAL INFORMATION:
APPLICANT: GOLDSPIRK, GEOFFREY
APPLICANT: TERENCE, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
FILE REFERENCE: 117-351
CURRENT APPLICATION NUMBER: US/09/852,261

CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GB 0011278.9
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1
LENGTH: 517
TYPE: DNA
ORGANISM: Homo sapiens
US-09-852-261-1

Query Match 60.3%; Score 325.2; DB 10; Length 517;
Best Local Similarity 81.2%; Pred. No. 4.1e-99;
Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;
QY 1 GGACCCAGAGACCCCTTTCGGGGCTGAGCTGTGAGAGCTCTTCAGTCTGTGTGACCA 60
Db 1 GGACCCAGAGAGCTCTCGGGTGTGAGCTGTGAGAGCTCTTCAGTCTGTGTGAGAG 60
QY 61 AGGGGCTTTTACTTCAACAGCCGACAGCTATGCTCCAGCATTCGAGAGGCAACACAG 120
Db 61 AGGGGCTTTTATTCAACAGCCGACAGCTATGCTCCAGCATTCGAGAGGCAACCTCAG 120
QY 121 ACAGGCACTGTGATGATGATGCTTCCGAGCTGTGATGATGATGATGATGATGATGAT 180
Db 121 ACAGGCACTGTGATGATGATGCTTCCGAGCTGTGATGATGATGATGATGATGATGAT 180
QY 181 TGATGCTGCTGCAAGCTTCAACAGCTGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 TGATGCTGCTGCAAGCTTCAACAGCTGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATGCCCAAGACTCGAAGTCCGAGCCCTATCCGACACAGAAAGAGAGCTGCAAGG 300
Db 241 ATGCCCAAGACTCGAAGTCCGAGCCCTATCCGACACAGAAAGAGAGCTGCAAGG 300
QY 301 AGAAGGAAGAGAGTACACTTGAAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AGAAGGAAGAGAGTACACTTGAAGAGACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CAGAGTGTAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 CAGAGTGTAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 CTGCTTGAAGACCTGCAAAACATCGAAGACCTGCAAAATATCAATATGATGATGATGAT 480
Db 421 CTGCTGACAGTGTACCTGATTAACATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 TCATTTAG 540
Db 481 TCATTTAG 540
QY 541 ACATTTCAAGAGT-GGCAATTTCCCGCAATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 ACATTTCAAGAGT-GGCAATTTCCCGCAATGATGATGATGATGATGATGATGATGATGAT 600

RESULT 6
US-10-136-639-4
Sequence 4, Application US/10136639
Patent No. US20030072761A1
GENERAL INFORMATION:
APPLICANT: Lebowitz, Jonathan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLO
FILE REFERENCE: SYM-008
CURRENT APPLICATION NUMBER: US/10/136,639
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 60/329,650
PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO: 4
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
US-10-136-639-4

Query Match 50.9%: Score 274.2; DB 9; Length 7260;
Best Local Similarity 76.0%: Pred. No. 2.7e-81;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

QY 1 GGACCAAGAGACCCCTTGGGGGGCTGAGCTGTGAGAGCCTCTTCAAGTGTGTGAGCA 60
DB 311 GGACCGAGAGAGCCTGTGGGGGGCTGAGCTGTGAGAGTGTCTTCAAGTGTGTGAGCA 370

QY 61 AGGGGCTTTTACTTCAACAAAGCCCAAGCTATGAGCTTCCAGGAGGAGGAGGAGGAGG 120
DB 371 AGGGGCTTTTATTTTCAACAAAGCCCAAGGAGTATGAGCTTCCAGGAGGAGGAGGAGG 430

QY 121 AGGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 431 AGGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490

QY 181 TGTGTCGGCTGCAAGCCTTCAACAAAGCTGATGATGATGATGATGATGATGATGATG 240
DB 491 TGTGTCGGCTGCAAGCCTTCAACAAAGCTGATGATGATGATGATGATGATGATGATG 550

QY 241 ATGCCCAAGACTCAGAAAGTCCAGCCCTATGACACACAGAAAGAAAGAGTGCAGAG 300
DB 551 ATGCCCAAGACTCAGAAAGTCCAGCCCTATGACACACAGAAAGAAAGAGTGCAGAG 565

QY 301 AGAAGAAAGAGTACACTTGAAGACACAGTGAAGAGTGCAGAGAAACAGACCTA 360
DB 566 -----AAGAAAGTACACTTGAAGACACAGTGAAGAGTGCAGAGAAACAGACCTA 618

QY 361 CAGAAATGTAGAGAGAGCCCTCCAGAGAAAGAAATGCGAGTCCAGGAGATCCCTTG 420
DB 619 CAGAAATGTAGAGAGAGCCCTCCAGAGAAAGTGAAGATGAGTCCAGGAGATCCCTTG 678

QY 421 --CTGCTTGAGCAACCTGCAAAACATCGAGACCTGCAAAATATCAATTAATGATGAA 478
DB 679 CTGCTTGAGCAACCTGCAAAACATCGAGACCTGCAAAACATGAAACATGATGAA 732

QY 479 TATCAATTTAGAGATGAGGATTTCCCTCAATGAATTAACAAAGTAAATATCC 531
DB 733 TATCAATTTAGAGATGAGGATTTCCCTCAATGAATTAACAAAGTAAATATCC 785

RESULT 7
US-09-919-497-24
Sequence 24, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Muller, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
US-09-919-497-24

Query Match 50.9%: Score 274.2; DB 10; Length 7260;
Best Local Similarity 76.0%: Pred. No. 2.7e-81;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

QY 1 GGACCAAGAGACCCCTTGGGGGGCTGAGCTGTGAGAGCCTCTTCAAGTGTGTGAGCA 60
DB 311 GGACCGAGAGAGCCTGTGGGGGGCTGAGCTGTGAGAGTGTCTTCAAGTGTGTGAGCA 370

QY 61 AGGGGCTTTTACTTCAACAAAGCCCAAGCTATGAGCTTCCAGGAGGAGGAGGAGGAGG 120
DB 371 AGGGGCTTTTATTTTCAACAAAGCCCAAGGAGTATGAGCTTCCAGGAGGAGGAGGAGG 430

QY 121 AGGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 431 AGGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490

QY 181 TGTGTCGGCTGCAAGCCTTCAACAAAGCTGATGATGATGATGATGATGATGATGATG 240
DB 491 TGTGTCGGCTGCAAGCCTTCAACAAAGCTGATGATGATGATGATGATGATGATGATG 550

QY 241 ATGCCCAAGACTCAGAAAGTCCAGCCCTATGACACACAGAAAGAAAGAGTGCAGAG 300
DB 551 ATGCCCAAGACTCAGAAAGTCCAGCCCTATGACACACAGAAAGAAAGAGTGCAGAG 565

QY 301 AGAAGAAAGAGTACACTTGAAGACACAGTGAAGAGTGCAGAGAAACAGACCTA 360
DB 566 -----AAGAAAGTACACTTGAAGACACAGTGAAGAGTGCAGAGAAACAGACCTA 618

QY 361 CAGAAATGTAGAGAGAGCCCTCCAGAGAAAGAAATGCGAGTCCAGGAGATCCCTTG 420
DB 619 CAGAAATGTAGAGAGAGCCCTCCAGAGAAAGTGAAGATGAGTCCAGGAGATCCCTTG 678

QY 421 --CTGCTTGAGCAACCTGCAAAACATCGAGACCTGCAAAATATCAATTAATGATGAA 478
DB 679 CTGCTTGAGCAACCTGCAAAACATCGAGACCTGCAAAACATGAAACATGATGAA 732

QY 479 TATCAATTTAGAGATGAGGATTTCCCTCAATGAATTAACAAAGTAAATATCC 531
DB 733 TATCAATTTAGAGATGAGGATTTCCCTCAATGAATTAACAAAGTAAATATCC 785

RESULT 8
US-09-880-107-3739
Sequence 3739, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherle, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3739
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025
US-09-880-107-3739

Query Match 50.9%: Score 274.2; DB 10; Length 7260;
Best Local Similarity 76.0%: Pred. No. 2.7e-81;
Matches 405; Conservative 0; Mismatches 68; Indels 60; Gaps 3;

QY 1 GGACCAAGAGACCCCTTGGGGGGCTGAGCTGTGAGAGCCTCTTCAAGTGTGTGAGCA 60
DB 311 GGACCGAGAGAGCCTGTGGGGGGCTGAGCTGTGAGAGTGTCTTCAAGTGTGTGAGCA 370

QY 61 AGGGGCTTTTACTTCAACAAAGCCCAAGCTATGAGCTTCCAGGAGGAGGAGGAGGAGG 120
DB 371 AGGGGCTTTTATTTTCAACAAAGCCCAAGGAGTATGAGCTTCCAGGAGGAGGAGGAGG 430

QY 121 AGGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 431 AGGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490

QY 181 TGTGTCGGCTGCAAGCCTTCAACAAAGCTGATGATGATGATGATGATGATGATGATG 240

DB 491 TGCCACACCCCTCAGACCTGCAAGTCACTGCTGCTCCGTGCGCCGCCACACCGAC 550
QY 241 ATGCCCAAGACTCAGAAATGCCACCCCTATCGACACACAGAAAGAAAGCTGCAAAAG 300
DB 551 ATGCCCAAGACCCAG-----565
QY 301 AGAAGAAAGGAATACACTTGAAGAACAGAGTGAAGAGGAAAGTGCAGAAAGACTTA 360
DB 566 -----AAGAAATACATTTTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618
QY 361 CAGATGTAG 420
DB 619 CAGATGTAG 678
QY 421 --CTGCTTGACAGACCTGCAAAACATGCGAAGACCTGCAAAATATCATATAGATTCAA 478
DB 679 CTCTGCAGAGAGTTACCTGTTAACTTGAACACCTTACA-----AAAAATAGATTGA 732
QY 479 TATCATTTAG 531
DB 733 TAAACATTTAAAGATGGGCGGTTTCCCCCATGAAATACAGATTAACATTC 785

RESULT 9
US-09-852-261-13
; Sequence 13, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFREY
; APPLICANT: TEREHNGH, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-852-261-13

Query Match 48.6%; Score 262; DB 10; Length 471;
Best Local Similarity 74.7%; Pred. No. 7.7e-78;
Matches 396; Conservative 0; Mismatches 75; Indels 59; Gaps 3;

QY 1 GGACCAAGAGACCCCTTTCGGGGGCTGAGCTGTGAGAGCTTCTGAGTTCTGCTGTGAGCA 60
DB 1 GGACCGGAGAGAGCTCTCGGTGCTGAGCTGTGAGATGCTTCAATTCGTGTGAGAGAC 60
QY 61 AGGGGCTTTTACTTCAACAAGCCACAGCTATAGCTCCAGCATTTGGAGGGGACACAG 120
DB 61 AGGGGCTTTTATTCAACAAGCCACAGATACGGCTCCAGAGTGGAGGGGACCTCAG 120
QY 121 ACGGGCATTTGATGATGATGCTGCTTCCGAGAGCTGTATGTGAGAGAGCTGGAGATGTAC 180
DB 121 ACGGGCATTCGATGATGATGCTGCTTCCGAGAGCTGTATGTGAGAGAGCTGGAGATGTAC 180
QY 181 TGTGTCGCTGCAAGCCTTACAAAGTCAAGTCTTCCATCCGGGCCAGGCCCACTGAC 240
DB 181 TGTGTCACCCCTCAAGCCGGAAGGCGAGCCGCTCCGTGCGTCCAGCCCAACCGAC 240
QY 241 ATGCCCAAGACTCGAAGTCCAGCCCTTATCGACACACAGAAAGAAAGCTGCAAAAG 300
DB 241 ATGCCCAAGACTCG-----255
QY 301 AGAAGAAAGGAATACACTTGAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 256 -----AAGAAATACATTTTGAAGAAACAGATAGAGAGAGAGAGAGAGAGAGAG 308

QY 361 CAGATGTAG 420
DB 309 CAGAGATGTAG 368
QY 421 CTGCTTGACAGACCTGCAAAACATGCGAAGACCTGCAAAATATCATATAGATTCAA 480
DB 369 CTCTGCAGAGTTACCTGTTAACTTGAACATTTGAGATFACCGGCCA-----AAAAATAGATTGATC 422
QY 481 TCATTTAG 530
DB 423 ACATTTCAAAAGAT-GGCATTTTCCCAATGAAATACAGATTAACATTC 471

RESULT 10
US-10-161-088-3
; Sequence 3, Application US/10161088
; Publication No. US2003007761A1
; GENERAL INFORMATION:
; APPLICANT: Parrow, Vendela
; APPLICANT: Rosengren, Linda
; TITLE OF INVENTION: NEW METHODS
; FILE REFERENCE: 13425-111001
; CURRENT APPLICATION NUMBER: US/10/161,088
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-088-3

Query Match 39.7%; Score 213.8; DB 9; Length 286;
Best Local Similarity 89.5%; Pred. No. 1e-61;
Matches 230; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 16 TCGGGGCTGAGCTGTGAGAGAGCTTCTGAGTTCTGATGTGAGACCAAGGGGCTTTACTTC 75
DB 18 TCGGGGCTGAGCTGTGAGAGAGCTTCTGAGTTCTGATGTGAGAGAGAGAGAGAGAGAG 77
QY 76 AACAAAGCCAGAGCTGTATGCTCCAGCATTCGAGAGGGGACACAGAGGGGCTTTGAT 135
DB 76 AACAAAGCCAGAGCTGTATGCTCCAGCATTCGAGAGGGGACACAGAGGGGCTTTGAT 137
QY 136 GAGTGTGCTTCCGAGAGCTGTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
DB 136 GAGTGTGCTTCCGAGAGCTGTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 197
QY 196 CCTACAAGTCAAGCTGTTCCATCCGGGGCCAGGGCCACACTGACATGCCAAGACTAG 255
DB 196 CCTACAAGTCAAGCTGTTCCATCCGGGGCCAGGGCCACACTGACATGCCAAGACTAG 257
QY 256 AAGTCCAGAGCCCTTATC 272
DB 256 GCATGCAAGCTGTCTC 274

RESULT 11
US-09-852-261-9
; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFREY
; APPLICANT: TEREHNGH, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-9

Query Match 38.4%; Score 206.8; DB 10; Length 318;
Best Local Similarity 87.6%; Pred. No. 2.5e-59;
Matches 226; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTGGCGGGGCTGAGCTGTGGAGCTCTTCAGTTCGTGTGACCA 60
DB 1 GGACCCGAGACGCTGCGGGGCTGAGCTGTGGAGCTCTTCAGTTCGTGTGAGAC 60
QY 61 AGGGGCTTTTACTTCAACAAGCCACAGCTATAGCTCAGATTCGAGGGGACCAAG 120
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QY 181 TGTGTCCTGCAAGCTTCAAAAGTACGCTGTTCCATCCGGGCCACGCTACACTGAC 240
DB 181 TGGGACCCCTCAAGGCTCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 ATGCCCAAGACTCAGAG 258
DB 241 ATGCCCAAGACCCAGAG 258

RESULT 12
US-10-238-114-1
; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
; APPLICANT: Meril
; APPLICANT: ANDREONI, Christine Michele
; TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST FELINE RE
; FILE REFERENCE: 454313-3165.1
; CURRENT APPLICATION NUMBER: US/10/238,114
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: FR 01 11736
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/318,666
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Felis catus
US-10-238-114-1

Query Match 37.8%; Score 203.6; DB 9; Length 462;
Best Local Similarity 86.8%; Pred. No. 3.6e-58;
Matches 224; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTGGCGGGGCTGAGCTGTGGAGCTCTTCAGTTCGTGTGACCA 60
DB 145 GGACCAAGACCCCTTGGCGGGGCTGAGCTGTGGAGCTCTTCAGTTCGTGTGACCA 204
QY 61 AGGGGCTTTTACTTCAACAAGCCACAGCTATAGCTCAGATTCGAGGGGACCAAG 120
DB 205 AGGGGCTTTTATTTCACAAGCCACAGGCTATAGCTCAGAGAGTGGAGGGGCTGAG 264
QY 121 ACGGGCAATGTGATGATGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
DB 265 ACAGGATCGTGTGATGATGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 324
QY 181 TGTGTCCTGCAAGCTTCAAAAGTACGCTGTTCCATCCGGGCCACGCTACACTGAC 240

DB 325 TGTGACCCCTCAAGCCCTGCCAAGTCTGCCGCTCACTGCTGCTCAAGCCGACACTGAC 384
QY 241 ATGCCCAAGACTCAGAG 258
DB 385 ATGCCCAAGGCTCAGAG 402

RESULT 13
US-09-930-377B-1
; Sequence 1, Application US/09930377B
; Patent No. US20020144296A1
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Matthew B.
; APPLICANT: Donovan, Sharon M.
; APPLICANT: Bleck, Gregory T.
; APPLICANT: Monaco-Seigel, Marcia
; TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
; FILE REFERENCE: 66-00
; CURRENT APPLICATION NUMBER: US/09/930,377B
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,474
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4532
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alpha-LA/IGF-I
US-09-930-377B-1

Query Match 30.5%; Score 164.6; DB 10; Length 4532;
Best Local Similarity 84.5%; Pred. No. 1.8e-44;
Matches 185; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GGACCAAGACCCCTTGGCGGGGCTGAGCTGTGGAGCTCTTCAGTTCGTGTGACCA 60
DB 2046 GGACCAAGACCCCTTGGCGGGGCTGAGCTGTGGAGCTCTTCAGTTCGTGTGAGAC 2105
QY 61 AGGGGCTTTTACTTCAACAAGCCACAGCTATAGCTCAGATTCGAGGGGACCAAG 120
DB 2106 AGGGGATTTTATTTCACAAGCCACAGGCTATGATCAGAGCTGAGAGGGGCTGAG 2165
QY 121 ACGGGCAATGTGATGATGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
DB 2166 ACAGGATCGTGTGATGATGTGCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAT 2225
QY 181 TGTGTCCTGCAAGCTTCAAAAGTACGCTGTTCCATC 219
DB 2226 TGGCACCCTCAAGGCTGCCAAGTCACTTGATGCTC 2264

RESULT 14
US-09-930-377B-2
; Sequence 2, Application US/09930377B
; Patent No. US20020144296A1
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Matthew B.
; APPLICANT: Donovan, Sharon M.
; APPLICANT: Bleck, Gregory T.
; APPLICANT: Monaco-Seigel, Marcia
; TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
; FILE REFERENCE: 66-00
; CURRENT APPLICATION NUMBER: US/09/930,377B
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,474
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 210

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DESCRIPTION: /desc = "Synthetic
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Search completed: June 15, 2003, 20:22:25
Job time : 99.6276 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:41:03 ; Search time 1146.61 Seconds
(without alignments)
7613.181 Million cell updates/sec

Title: US-09-852-261-3

Perfect score: 539

Sequence: 1 ggacacagacaccccttcggc.....agtaacatcccggaattc 539

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
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12: gb_est3:*
13: gb_est4:*
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16: em_estlun:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_tun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	501.6	93.1	549	9	A1169253 EST215088
C 2	469.2	87.1	558	9	A1503976 vm33d08.x
C 3	453.4	84.1	623	10	AM146128 um37e10.x
C 4	450.4	83.6	468	9	A1169770 EST215669
C 5	446.8	82.9	558	9	A1265629 u10ab07.x
C 6	437	81.1	653	14	BQ200567 U1-R-D21-BQ200567

Result 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
A1169253	EST215088	Normalized rat kidney, Banto Soares Rattus sp. cDNA clone	A1169253	A1169253.1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R., and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.
A1169253	EST215088	Normalized rat kidney, Banto Soares Rattus sp. cDNA clone	A1169253	A1169253.1	GI:4134375	EST	Rattus sp.	1 (bases 1 to 549)	Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kariyave, A.R., and Adams, M.D.	Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index	Unpublished (1998)	On Oct 6, 1998, this sequence version replaced gi:3705561.

ALIGNMENTS

FEATURES

Location/Qualifiers

source 1. 549
 /organism="Rattus sp."
 /db_xref="taxon:10118"
 /clone="RK18P33"
 /clone_lib="Normalized rat kidney, Bento Soares"
 /note="Organ: kidney; Vector: p713pac; Site_1: EcoRI;
 Site_2: NotI"
 BASE COUNT 112 a 140 c 133 g 164 t
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 Query Match 93.1%; Score 501.6; DB 9; Length 549;
 Best Local Similarity 97.3%; Pred. No. 2e-18;
 Matches 510; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Db 8 AGACCTTTGGGGGCTGAGCTGTGAGCTCTTCACTGTGTGTGACCAAGGCT 67
 549 AGACCTTTGGGGGCTGAGCTGTGAGCTCTTCACTGTGTGTGACCAAGGCT 490
 QY 68 TTTACTTCAACAAGCCACAGTCTATGCTCCAGATTGAGGGCACCACAGAGGCA 127
 Db 489 TTTACTTCAACAAGCCACAGTCTATGCTCCAGATTGAGGGCACCACAGAGGCA 430
 QY 128 TTGTGATGAGTGTCTTCCGAGCTGATCTGAGAGGCTGAGATGTCTGTCC 187
 Db 423 TTGTGATGAGTGTCTTCCGAGCTGATCTGAGAGGCTGAGATGTCTGTCC 370
 QY 188 GCTGACAGCTCAAAAGTCAAGTCTGTTCCATCCGGGCGCCACACATGACATGCCA 247
 Db 369 CGCTGAAGCTCAAAAGTCAAGTCTGTTCCATCCGGGCGCCACACATGACATGCCA 310
 QY 248 AGACTTCAGAGTCCCAAGCTTATGACACACAGAAAGAAAGTCCAAAGAGAGA 307
 Db 309 AGACTTCAGAGTCCCAAGCTTATGACACACAGAAAGAAAGTCCAAAGAGAGA 250
 QY 308 AAGGAAGTCACTTGAAGACACAAAGTAGAGAGAGTCAAGAACAGACCTACGAATG 367
 Db 249 AAGGAAGTCACTTGAAGACACAAAGTAGAGAGAGTCAAGAACAGACCTACGAATG 190
 QY 368 TAGGAGAGAGTCCCGAGACAGAAATGCCAGCTCACCAGATCTTGTGCTTG 427
 Db 189 TAGGAGAGAGTCCCGAGACAGAAATGCCAGCTCACCAGATCTTGTGCTTG 130
 QY 428 AGCAACCTGCAAAACATCGAAGACCTGCAATATGATATGATCAATATTC 487
 Db 129 AGCAACCTGCAAAACATCGAAGACCTGCAATATGATATGATCAATATTC 70
 QY 488 AGAGATGGGCAATTTCCCTCAATGAATACACAAGTAACATTC 531
 Db 69 AGAGATGGGCAATTTCCCTCAATGAATACACAAGTAACATTC 26
 RESULT 2
 A1503976/c 558 bp mRNA linear EST 11-MAR-1999
 LOCUS vm43d08.x1 Striatum mouse diaphragm (#937303) Mus musculus cDNA
 DEFINITION clone IMAGE:1001007 3' similar to gb:U04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
 ACCESSION A1503976
 VERSION A1503976.1 GI:4401827
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 558)
 * AUTHORS
 Marta, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Stepien, K., Thelning, B., Allen, M., Bowers, T., Person,
 B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schuck, R., Ritter,
 E., Korn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R., and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Marta M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:565223
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 High quality sequence stop: 440.
 Location/Qualifiers
 1. 558
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:1001007"
 /clone_lib="Striatum mouse diaphragm (#937303)"
 /tissue_type="diaphragm"
 /dev_stage="adult"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
 prepared from diaphragm muscle. Primer: Oligo dt. Average
 insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor
 sequence: 5' GAATTCGACAG 3' -3' adaptor sequence: 5'
 CTCGAGCTTTTCTTTTCTTTT 3'"
 BASE COUNT 103 a 133 c 149 g 173 t
 ORIGIN
 Query Match 87.1%; Score 469.2; DB 9; Length 558;
 Best Local Similarity 92.8%; Pred. No. 2e-119;
 Matches 492; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 QY 1 GGACAGAGACCCCTTGGGGGCTGAGCTGTGAGCTCTTCACTGTGTGTGACCA 60
 Db 530 GGACAGAGACCCCTTGGGGGCTGAGCTGTGAGCTCTTCACTGTGTGTGACCG 471
 QY 61 AGGGCTTTTACTTCAACAAGCCCAAGTCTATGCTCCAGATTCGGAGGACACACAG 120
 Db 470 AGGGCTTTTACTTCAACAAGCCCAAGTCTATGCTCCAGATTCGGAGGACACACAG 411
 QY 121 ACGGCAATGTGATGATGTGTGCTTCCGAGCTGTGATCTGAGAGAGCTGAGATGTAC 180
 Db 410 ACGGCAATGTGATGATGTGTGCTTCCGAGCTGTGATCTGAGAGAGCTGAGATGTAC 351
 QY 181 TGTGTCCGCTCAAGCCCTACAAAGTCAAGTCTGTTCCATCCGAGGCGCCACACTGAC 240
 Db 350 TGTGTCCGCTCAAGCCCTACAAAGTCAAGTCTGTTCCATCCGAGGCGCCACACTGAC 291
 QY 241 ATGCCCAAGACTCAAGTCTCCAGCCCTATCCAGACACAGAAAGAAAGAGCTGCAAGG 300
 Db 290 ATGCCCAAGACTCAAGTCTCCAGCCCTATCCAGACACAGAAAGAAAGAGCTGCAAGG 231
 QY 301 AGAAGGAAGGAAGTACACTTGAAGACACAGAGTGAAGAGTGCAGAGAAAGACTA 360
 Db 230 AGAAGGAAGGAAGTACACTTGAAGACACAGAGTGAAGAGTGCAGAGAAAGACTA 171
 QY 361 CAGAAATGAGAGAGAGCTCCCGAGAGACAGAAATGCCAGTCCGAGAGATCTTTG 420
 Db 170 CAGAAATGAGAGAGAGCTCCCGAGAGACAGAAATGCCAGTCCGAGAGATCTTTG 111
 QY 421 CTGCTTGAAGCACTGCAAAACATCGAGACAGCTGCCCAATATCAATAGATGCATA 480
 Db 110 CTGCTTGAAGCACTGCAAAACATCGAGACAGCTGCCCAATATCAATAGATGCATA 51
 QY 481 TCATTTAGAGATGGCATTTCCCTCAATGAATACACAAGTAACATTC 530
 Db 50 ACATTAACAAGATGGGCAATTTCCCGCAATGAATATCAAGTAACATTC 1
 RESULT 3
 A146128/c 623 bp mRNA linear EST 10-OCT-2000
 LOCUS A146128

```

DEFINITION  um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
              IMAGE:2247498.3' similar to gb:X04482 Mouse mRNA for
              preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AM146128
VERSION     AM146128.1  GI:6167864
KEYWORDS    EST.
SOURCE      house mouse.
            Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 623)
            Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
            Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
            , B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
            , E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
            Waterston, R., and Wilson, R.
            The WashU-NCI Mouse EST Project 1999
            Unpublished (1999)
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MG:1006958
            Seq primer: custom primer used
            High quality sequence step: 499.
FEATURES
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        /strain="C57BL"
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        /clone="IMAGE:2247498"
        /clone_lib="Sugano mouse embryo mewa"
        /dev_stage="embryo, 14 dpc"
        /lab_host="DH10B"
        /note="Vector: pME18S-FL3; Site_1: DraIII (CAGCTGTG);
        /note="Site_2: DraIII (CAGCATGTG); 1st strand cDNA was primed
        with an oligo(dT) primer [ATGCGGCCCTTTTCTTTTCTTTT];
        double-stranded cDNA was ligated to a DraIII adaptor
        [CTCTGGCCTACTGG], digested and cloned into a DraIII adaptor
        sites of the pME18S-FL3 vector (3' site CAGCTGTG, 3' site
        CAGCATGTG). XhoI should be used to isolate the cDNA
        insert. Size selection was performed to exclude fragments
        <1.5kb. Library constructed by Dr. Sumio Sugano
        (University of Tokyo Institute of Medical Science).
        Custom primers for sequencing: 5' end primer
        CTCTCGCTCTTAAAGCTGCG and 3' end primer
        CGACCTGACGTGAGCACA."
BASE COUNT  123 a 138 c 170 g 191 t 1 others
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Query Match      84.1%; Score 453.4; DB 10; Length 623;
Best Local Similarity 92.1%; Pred. No. 5,1e-115;
Matches 489; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
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2 |||||||
3 541 GGACCAAGAGACCTTTTCGGGGCTGAGCTGGTGACGCTCTTCAAGTCTGTGTGACCG 482
4 |||||||
5 61 AGGGGCTTTTACTCAACAGCCACAGTCTATGCGTCCAGCATTCGGAGGACACCAAG 120
6 |||||||
7 481 AGGGGCTTTTACTCAACAGCCACAGTCTATGCGTCCAGCATTCGGAGGACACCTCAG 422
8 |||||||
9 121 ACGGGCAATTGTGATGAGTGTGCTTCGAGCTGTGATCTGAGGAGCTGAGATGTAC 180
10 |||||||
11 421 ACAGGCAATTGTGATGAGTGTGCTTCGAGCTGTGATCTGAGGAGCTGAGAAATGTAC 362
12 |||||||
13 181 TGTGTGCGCTGACAGCTTACAAATGACGTCGTTCCATCCGGGCGCCACGACACACATGAC 240
14 |||||||
15 361 TGTGTGCGCTGACAGCTTACAAATGACGTCGTTCCATCCGGGCGCCACGACACATGAC 302

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QY 241 ATGCCCAAGACTAGAGTCCAGCCCTTATCGACACAGAAAGAAAGCTGCAAGG 300
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DB 241 AGAAGGAAGAGTACACTGAGTGAAGAACAGTATAGGAGTGCAGAAACAGACCTA 182
QY 361 CAGATGTAGAGAGACCTCCCGAGAGACAGAAATATGACAGTCCAGGAGATCCTTTG 420
DB 181 CAGATGTAGAGAGAGACCTCCCGAGAGAGAGAAATATGACAGTCCAGGAGATCCTTTG 122
QY 421 CTGCTTGAGACACTGCAAAACATCGAGACACTGCGCAATATGATGATTAATAA 480
DB 121 CTGCTTGAGACACTGCAAAACATCGAGACACTGCGCAATATGATGATTAATAA 62
QY 481 TCATTTCAGAGATGGCATTTCCCTCATGATGAATACAGTAATGATTC 531
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RESULT 4
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LOCUS EST215669 Normalized rat liver, Bento Soares Rattus sp. cDNA clone
DEFINITION RIAT07.3' end, mRNA sequence.
ACCESSION A1169770
VERSION A1169770.1 GI:3709810
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 468)
            Lee, N.H., Glodde, A., Chandra, I., Mason, T.M., Quackenbush, J.,
            Kerlavage, A.R. and Adams, M.D.
            Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
            Unpublished (1998)
            Other-ESTs: TC50779
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@igf.org
            Seq primer: M13-21.
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        /db_xref="taxon:10118"
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        /clone_lib="Normalized rat liver, Bento Soares"
        /note="Organ: liver; Vector: pT73pac; Site_1: EcoRI;
        Site_2: NotI"
BASE COUNT  85 a 115 c 119 g 149 t
ORIGIN
Query Match      83.6%; Score 450.4; DB 9; Length 468;
Best Local Similarity 97.6%; Pred. No. 3,1e-114;
Matches 457; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
63 GGGCTTTTACTCAACAGCCACAGTCTATGCTCCAGCATTCGGAGGACACCAAGAC 122
DB 468 GGGCTTTTACTCAACAGCCACAGTCTATGCTCCAGCATTCGGAGGACACCAAGAC 409
QY 123 GGGCATTTGTGATGAGTGTGCTTCGAGCTGTGATCTGAGAGAGCTGGAATGTACTG 182
DB 408 GGGCATTTGTGATGAGTGTGCTTCGAGCTGTGATCTGAGAGAGCTGGAATGTACTG 349

```


RESULT 5				
AI265629/c				
LOCUS	AI265629	558 bp	MRNA	linear EST 18-NOV-1996
DEFINITION	U10407.1 x1 Sugano mouse liver mla Mus musculus CDNA clone			
	IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for			
	preproinsulin-like growth factor IB (MOUSE); mRNA sequence.			
ACCESSION	AI265629			

FEATURES
 SOURCE
 TITLE
 JOURNAL
 COMMENT
 REFERENCE
 AUTHORS
 ORGANISM
 SOURCE
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 1 (bases 1 to 558)
 Mairr,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
 Theiling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Karra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:975225
 Seq primer: custom primer used.
 High quality sequence stop: 495.
 Location/Qualifiers
 1..558

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/organism="Mus musculus"  
/strain="C57BL"  
/db_xref="taxon:10090"  
/clone_image=1890901  
/clone_id="Sugano mouse liver mlia"  
/sex="female"  
/dev_stage="adult"  
/lab_host="DH10B"  
  
name=Organ; site: Vector: pME18s-FL3; Site_1: DraIII  
(CACGCTGGT); Site_2: DraIII (CACCATGTG); 1st strand cDNA  
was primed with an oligo(dT) primer  
[ATGTCGCGTTTTTTTTTTTTTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor [TGTTGCGCTACTGG], digested
```

BASE COUNT
ORIGIN

106 a 135 c 156 g 161 t

Query Match	82.9%	Score 446.8	DB 9	Length 558
Best Local Similarity	92.7%	Pred. No. 3.3e-113		
Matches 469	Conservative 0	Mismatches 37	Indels 0	Gaps 0
Qy 1	GGACCAGAGACCCTTTGCGGGGCTGAGCTGTGTGAGCCCTTCATGTTGTGTGTGACCA	60		
Dp 506	GGACCCAGAGACCCTTTGCGGGGCTGAGCTGTGTGATGCTCTTCAGTTGTGTGTGACCG	447		
Qy 61	AGGGGCTTTTACTTCACAAAGCCACAGTCTATGGCTCCAGCATTCGGAGGGGCACCAG	120		
Dp 446	AGGGGCTTTTACTTCACAAAGCCACAGGCTATGGCTCCAGCATTCGGAGGGGCACCTAG	387		
Qy 121	ACGGGCAATTGGATGATGTGTGCTTCGGAGCTGTGATCTGGAGAGGCTGGAATGTAC	180		
Dp 386	ACAGGCATTTGGGTGTGATGTGTGCTTCGGAGCTGTGATCTGAGAGACTGTGAAATGTAC	327		
Qy 181	TGTGTCCGCTGCAAGCCCTCAAAAGTCAAGTGTTCATCCGGGCCCAAGCCGACACTGAC	240		
Dp 326	TGTGCCCCACTGAAGCCTCAAAAGCAGCCCGCTCTATCCGTGCCAGCGCACACTGAC	267		
Qy 241	ATGCCCAAGACTCGAAGTCCCAAGCCCTATCGACACACAAGAAAGAGAGCTCCAAAG	300		
Dp 266	ATGCCCAAGACTCGAAGTCCCGCTCCCTACTCGACAAACAGAAAGAGAACTCCAAAG	207		
Qy 301	AGAAGGAAAGAACTTACCTGAGACACACAGTAGAGGAAGTCCAGAGCAACAGACCTA	360		
Dp 206	AGAAGGAAAGAACTTACCTTGAAGACACACAGTAGAGGAAGTCCAGAGCAACAGACCTA	147		
Qy 361	CAGATGTAGAGAGAGCCTCCCGAGGAACAGAAATGCGACGTCCAGCGCAAGATCCTTTG	420		
Dp 146	CAGATGTAGAGAGAGCCTCCCGAGGAGAGAAATGCGACATCCAGCGCAGATCCTTTG	87		
Qy 421	CTGCTTGAGCAACTGCAAAACATCGAACCCTGCCAAATATTAATATAGATTCAATA	480		
Dp 86	CTGCTTGAGCAACTGCAAAACATCGAACAACCTTACCAAAATATTAATATAGTCCATA	27		
Qy 481	TCATTTGAGATGGGCATTTCCCTC 506			
Dp 26	ACATTTCAAGATGGGCATTTTCCCCC 1			

RESULT	6
BQ200567/c	
LOCUS	BCQ200567 653 bp mRNA linear EST_02-MAY-2002
DEFINITION	UI-R-D2I-one-a-18-0-U sl UI-R-D2I Rattus norvegicus cDNA clone
ACCESSION	BQ200567
VERSION	BQ200567.1 GI:20417032
KEYWORDS	EST.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE	Rattus. 1 (bases 1 to 653)
AUTHORS	Bonaldi,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL MEDLINE	Genome Res. 6 (9), 791-806 (1996) 9704447
COMMENT	Contact: Soares, MB Program for Rat Gene Discovery and Mapping

University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized cartilaginous tumor library cDNA library preparation.
M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-43,
>AT-rich#low-complexity 118-164, >POLY_A*simple_repeat
Seq primer: M13 Forward
POLY-A=yes

FEATURES

SOURCE

Location/Qualifiers
1..653
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-D21-cne-a-18-0-U"
/tissue="fibroblast"
/dev_stage="37 days"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Spine; Vector: pTZ19-D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; UI-R-D21 is a normalized cDNA library containing the following tissue(s): Swam Rat Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTZ19-D-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTGTGA. The Rat cartilaginous tumor tissue was provided by Dr Jeff Stevens at the University of Iowa.
TAG-LIB=UI-R-D21
TAG-TISSUE=cartilaginous tumor
TAG-SEQ=CATCTGTGA"

BASE COUNT 134 a 137 c 137 g 245 t

Query Match 81.1%; Score 437; DB 14; Length 653;
Best Local Similarity 97.6%; Pred. No. 1,9e-110;
Matches 454; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

67 TTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGGAGGCGACACAGCGGC 126
653 TTTTACTTCAACAAGCCACAGTATGCTCCAGCATTTGGAGGCGACACAGCGGC 594
127 ATTGTGATGAGTGTCTCCGAGGTGATGCTGAGAGGCTGGAGATGATCTGTGTC 186
593 ATTGTGATGAGTGTCTCCGAGGTGATGCTGAGAGGCTGGAGATGATCTGTGTC 535
187 CGGTGAGGCTTACAAAGTACGCTGTTCCATCCGGGCCAGGCCACATGACATGCC 246
534 CGGTGAGGCTTACAAAGTACGCTGTTCCATCCGGGCCAGGCCACATGACATGCC 475
247 AAGCTCAGAGTCCCGCCCGCCATATGACACACAAGAAAGAGTGCACAAAGAGG 306
474 AAGCTCAGAGTCCCGCCCGCCATATGACACACAAGAAAGAGTGCACAAAGAGG 415
307 AAAGAGTACACTTGAAGAACACAAAGTACAGAGTGCAGAAAGAGTACAGAGT 366
414 AAAGAGTACACTTGAAGAACACAAAGTACAGAGTGCAGAAAGAGTACAGAGT 355
367 GTAGAGAGAGCTCCGAGGACAGAAATGCGACGTCACCGCAGATCTTGTGCTT 426

Db 354 GTAGAGAGAGCTCCGAGGACAGAAATGCGACGTCACCGCAGATCTTGTGCTT 295
Qy 427 GAGCAACCTGCAAAACATCGGAACACCTGCGCAATATCATATGATTCATATCATTT 486
Db 294 GAGCAACCTGCAAAACATCGGAACACCTGCGCAATATCATATGATTCATATCATTT 235
Qy 487 CGAGATGGGCAATTCCTCATGAAATACAGAAATCATTC 531
Db 234 CGAGATGGGCAATTCCTCATGAAATACAGAAATCATTC 190

RESULT 7
BF383724
LOCUS
DEFINITION
602044632F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4194295 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 594)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9527 row: p column: 08
High quality sequence stop: 589.

FEATURES

SOURCE

Location/Qualifiers
1..594
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4194295"
/clone_lib="NCI_CGAP_L19"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 175 a 162 c 142 g 115 t

Query Match 80.1%; Score 431.8; DB 12; Length 594;
Best Local Similarity 92.4%; Pred. No. 5e-109;
Matches 455; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

1 GAGCAGAGACCCCTTTCGGGGCTGAGCTGAGACGCTTCATGCTGTGTGGACCA 60
93 GAGCAGAGACCC -TTGCGGGGCTGAGCTGAGATGCTTCATGCTGTGTGGACCG 151
61 AGGGGTTTACTTCAACAAGCCACAGTCTGTGCTCCAGATCGGAGGCGACACAG 120
152 AGGGGTTTACTTCAACAAGCCACAGTCTGTGCTCCAGATTCGGAGGCGACCTG 211
Qy 121 ACGGGATTTGATGAGTGTGCTTCGAGCTGATCTGAGAGGCTGAGATGATAC 180
Db 212 ACGGGATTTGATGAGTGTGCTTCGAGCTGATCTGAGAGGCTGAGATGATAC 271
Qy 181 TGTGTCCGTTGAGAGTGTGCTTCATTCGAGGCGGCGACGCTACACTGAC 240
Db 272 TGTGTCCGTTGAGAGTGTGCTTCATTCGAGGCGGCGACGCTACACTGAC 331

performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTCTCTCTAAAGCTGG and 3' end primer CGACCTGCAGCTCGACCA."

BASE COUNT 127 a 154 c 175 g 185 t 1 others

Query Match 78.1%; Score 421.2; DB 9; Length 642;
Best Local Similarity 91.1%; Pred. No. 4.5e-106;
Matches 458; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 2 GACCAAGACCCCTTTCGCGGCTGAGCTGTGAGAGCTCTTCAAGTTCGTGTGACCA 61
DB 503 GACCAAGACCCCTTTCGCGGCTGAGCTGTGAGAGCTCTTCAAGTTCGTGTGACCA 444
QY 62 GGGGCTTTTACTCACAAGCCACAGTCTATGGCTCCAGCATTTGGAGGACCA 121
DB 443 GGGGCTTTTCTTCAACAAGCCACAGTCTATGGCTCCAGCATTTGGAGGACCA 384
QY 122 CGGGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 383 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
QY 181 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 240
DB 323 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 264
QY 241 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 300
DB 263 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 204
QY 301 AAGAGAAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 360
DB 203 AAGAGAAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 144
QY 361 CAGATGTAGAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 420
DB 143 CAGATGTAGAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 84
QY 421 CTGCTTGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 480
DB 83 CTGCTTGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 24
QY 481 TCATTTCAGAGAGGCAATTTC 503
DB 23 ACATTTCAGAGAGGCAATTTC 1

RESULT 11 525 bp mRNA linear EST 09-MAR-1999
AA963258
LOCUS UI-R-E1-9h-f-04-0-UI s1 UI-R-E1 Rattus norvegicus cDNA clone
DEFINITION UI-R-E1-9h-f-04-0-UI 3', mRNA sequence.

ACCESSION AA963258
VERSION AA963258.1 GI:4278182
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 525)

REFERENCE 1 (bases 1 to 525)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On May 18, 1998 this sequence version replaced gi:3136750.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult 12-day-embryo library. cDNA library preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics
Seq primer: M13 Forward
Location/Qualifiers
1. 525

FEATURES
source
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-E1-9h-f-04-0-UI"
/clone_1lb="UI-R-E1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-E1
library is a subtracted library derived from the UI-R-E0
library. The UI-R-E0 library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-E1) was constructed as follows: PCR
amplified cDNA inserts from a pool of UI-R-E0 clones from
which 3' ESTs had been derived was used as a driver in a
hybridization with the UI-R-E0 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-E1
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996).

BASE COUNT 107 a 133 c 126 g 159 t

Query Match 74.7%; Score 402.6; DB 9; Length 525;
Best Local Similarity 88.5%; Pred. No. 6e-101;
Matches 470; Conservative 0; Mismatches 9; Indels 52; Gaps 1;

QY 1 GGACCAAGACCCCTTTCGCGGCTGAGCTGTGAGAGCTCTTCAAGTTCGTGTGACCA 60
DB 521 GGACCAAGACCCCTTTCGCGGCTGAGCTGTGAGAGCTCTTCAAGTTCGTGTGACCA 462
QY 61 AGGGCTTTTACTCACAAGCCACAGTCTATGGCTCCAGCATTTGGAGGACCA 120
DB 461 AGGGCTTTTACTCACAAGCCACAGTCTATGGCTCCAGCATTTGGAGGACCA 402
QY 121 ACGGCAATTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 401 ACGGCAATTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342
QY 181 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 240
DB 341 TGTGTCCGCTGCAAGCTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 282
QY 241 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 300
DB 281 ATGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 267
QY 301 AAGAGAAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 360
DB 266 -----AAGAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 214
QY 361 CAGATGTAGAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 420
DB 213 CAGATGTAGAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 154

	AA945553/c	AA945553	EST201052	Normalized rat liver, Bencio Soares	EST 08-JAN-1999
LOCUS	AA945553/c	AA945553	EST201052	Normalized rat liver, Bencio Soares	EST 08-JAN-1999
DEFINITION			RLJA083 3' end, mRNA sequence.		
ACCESSION		AA945553			
VERSION		AA945553.1	GI:4132547		
KEYWORDS		EST.			
SOURCE		Rattus sp.			
ORGANISM		Rattus sp.			

REFERENCE	(pages 1 to 500)
AUTHORS	Iee,N.H. Gloder,A., Chandra,I., Mason,T.M., Quackenbush,J.,
TITLE	Kerlavage,A.R. and Adams,M.D.
JOURNAL	Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat
COMMENT	Gene Index
	Unpublished (1998)
	On May 1, 1998 this sequence version replaced g1::3105469.

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel.: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

```

FEATURES
  source
    1. 500 location/qualifiers
      /organism="Rattus sp."
      /db_xref="taxon:10118"
      /clone="RLA083"
      /clone_1fb="Normalized rat liver, Bento Soares"
      /note="Organ: liver; Vector: pTT3pac; Site_1: EcoRI
      Site_2: NotI"
BASE COUNT
  99 a 129 c 130 g 142 t
ORIGIN

```

Query Match	74.58;	Score 401.6;	DB 9;	Length 500;
Best Local Similarity	88.58;	Pred. No. 1.1e-100;		
Matches 469; Conservative	0;	Mismatches 9;	Indels 52;	Gaps 1

QY	1	GGAGCCAGAAACCCCTTTGGCGGGCTGAGCTGGAGCAAGCCTTCACATGGTGGTGGACCA	60
Db	478	GGAGCCAGAAACCCCTTTGGCGGGCTGAGCTGGAGCAAGCCTTCACATGGTGGTGGACCA	411
QY	61	AGGGCGTTTACTTCAACAAGCCACAGTCTATGCGTCCAGCATTTGGAGGGCACACCAG	121
Db	418	AGGGCGTTTACTTCAACAAGCCACAGCCTATGCGTCCAGCATTTGGAGGGCACACCAG	351
QY	121	ACGGCGATTGTGGATAGTGTGGCTTCGGAGACTGTGATGTAGAGAGGCTGGAGATGTAC	181
Db	358	ACGGCGATTGTGGATAGTGTGGCTTCGGAGACTGTGATGTAGAGAGGCTGGAGATGTAC	291
QY	181	TGTGTCCGCTGCAAGCCTACAAAGTCAGCTGTTCCATCCGGGCCAGCGCACACTGAC	241
Db	298	TGTGTCCGCTGCAAGCCTACAAAGTCAGCTGTTCCATCCGGGCCAGCGCACACTGAC	231
QY	241	ATGCCCCAAGACTACAGATGCCAGGCCCATGACACACAAAGAAAGAAAGACTGCAAAGG	301
Db	238	ATGCCCAAGACTACG-----22	361
QY	301	AGAAAGAAAGAGTACACTTGAAGAACCAAGTAAAGAAAGTCCAGAAACAAGACCTTA	361

Db	223	-----TAGGAGAGTACACTTGAAAGAACACAAGTGTAGAGAAAGTGCAGGAAACAGACCTA	171
Qy	361	CAGAAATGAGAGAGAGCCTCCCGAGGAACAGAAAATGCGACGTCACCCGCAAGATCCTTTG	420
Db	170	CAGAAATGAGAGAGAGAGCCTCCCGAGGAACAGAAAATGCGACGTCACCCGCAAGATCCTTTG	111
Qy	421	CTGCTTGAGCAACCTGCAAAACATGGGAACACACCTGCCAAATATCAATATAGTTCATAA	480
Db	110	CTGCTTGAGCAACCTGCAAAACATGGGAACACACCTGCCAAATATCAATATAGTTCATAA	51
Qy	481	TCATTTGAGAGATGGGCAATTCCTCCATGAAATACACAGAAACATTC	530
Db	50	CCATTTGAGAGATGGGCAATTCCTCCATGAAATACACAGAAACATTC 1	

RESULT	13			
LOCUS	AI599751/c			
DEFINITION	AI599751	525 bp	mrna	linear
ACCESSION	EST251443	Normalized rat embryo,	Bento Soares	Rattus sp. cDNA clone
VERSION	AI599751	3	end,	mrna sequence.
KEYWORDS	AI599751.1	GI:4608799		
SOURCE	EST.			
ORGANISM	Rattus sp.			
	Rattus sp.			

REFERENCE	1 (pages 1 to 525)
AUTHORS	Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE	Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat
JOURNAL	Gene Index
COMMENT	Unpublished (1998)
	Contact: Lee, NH

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel.: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@igf.org
Seq primer: M13-21.

FEATURES	
source	location/qualifiers
1. 525	
/organism="Rattus sp."	
/db_xref="taxon:10118"	
/clone="REMEG86"	
/clone_lib="Normalized rat embryo, Bento Soares"	
/dev_stage="embryo 8, 12, 18 dpc"	
/note="Vector: p713pac; Site_1: ECORI; Site_2: NOTI"	
BASE COUNT	107 a 133 c 140 g 145 t
ORIGIN	

Query Match	74.1%	Score 399.4	DB 9	Length 525
Best Local Similarity	88.1%	Pred. No. 4,7	Indels 10	
Matches 466	Conservative 0	Mismatches 11	Gaps 52	
QY	1	GGACCAAGACCCCTTTGCGGGGCTGACCTGATGAGCCTCTTCACTGTCGTGTGACCA	60	
Db	480	GGACCAAGACCCCTTTGCGGGGCTGACCTGATGAGCCTCTTCACTGTCGTGTGACCA	421	
QY	61	AGGGGCTTTTACTTCACCAAGCCACAGTCATGGCTCCAGCATTCGAGGGCCACCAAG	120	
Db	420	AGGGGCTTTTACTTCACCAAGCCACAGTCATGGCTCCAGCATTCGAGGGCCACCAAG	361	
QY	121	ACGGGCACTTGTGATGATGAGTGTGCTTCCGAGCTGTATCTGAGGAGGCTGGAGATGTAC	180	
Db	360	ACGGGCACTTGTGATGATGAGTGTGCTTCCGAGCTGTATCTGAGGAGGCTGGAGATGTAC	301	
QY	181	TGTGTCCGCTGCAAGCCCTACAAATCCAGCTGTCCATCCGGGGCCACGCGCACTATGAC	240	
Db	300	TGTGTCCGCTGCAAGCCCTACAAATCCAGCTGTCCATCCGGGGCCACGCGCACTATGAC	241	

QY 241 ATGCCAGACTCAGAGTCCAGCCCTATCGACACAGAGAAAGAGCTGCAAGG 300
 |||||
 Db 240 ATGCCAGACTCAG----- 226
 QY 301 AGAGAGAAAGAGTACTTAAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 360
 |||||
 Db 225 -----AAGGAGAGTACTTAAAGACACAGTAGAGAGAGTGCAGAAACAGACCTA 173
 QY 361 CAGATGTAGAGAGAGCCCTCCGAGAGACAGAAATGCCAGCTACCCGCAATCTTGG 420
 |||||
 Db 172 CAGAGTGTAGAGAGAGCCCTCCGAGAGACAGAAATGCCAGCTACCCGCAATCTTGG 113
 QY 421 CTGCTTGAACCACTGCAAAACATCGAGACACCTGCCAATATCATATATGAGTTCAATA 480
 |||||
 Db 112 CTGCTTGAACCACTGCAAAACATCGAGACACCTGCCAATATCATATATGAGTTCAATA 53
 QY 481 TCATTTCAGAGATGGGCTATTCCTCAATGAATACACAGTAACATTCC 531
 |||||
 Db 52 CCATTTCAGAGATGGGCTATTCCTCAATGAATACACAGTAACATTCC 2

RESULT 14
 BI294072/c 499 bp mRNA linear EST 19-JUL-2001
 LOCUS UI-R-DK0-cej-b-03-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone
 DEFINITION BI294072
 UI-R-DK0-cej-b-03-0-UI 3', mRNA sequence.
 ACCESSION BI294072
 VERSION BI294072.1 GI:14956179
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 499)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: mscares@blue.weeg.uiowa.edu

The sequence contained an oligo-dt track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dt track served to identify it as a clone from the
 normalized rat heart pool library cDNA library Preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLY-A=yes.

FEATURES

Source Location/Qualifiers
 1..499
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone_1db="UI-R-DK0-cej-b-03-0-UI"
 /dev_stage="ADULT"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pUT3D-Pac (Pharmacia) with a modified
 polylinker. Site1: Not I; Site2: Eco RI; The UI-R-DK0
 library is a subtracted library derived from a mixture of
 five individually tagged normalized rat libraries:
 brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%),
 aorta-nRBP (20%), and placenta-nRBP (20%). Each original
 library was constructed from a mixture of equal amounts of

RNA from seven different developmental time-points:
 embryonic day 17, embryonic day 19, embryonic day 21,
 adult day 1, adult day 12, adult day 75, and adult day
 200. (Exception: the aorta pool does not contain embryonic
 day 17 RNA and the placenta pool contains only the three
 embryonic stages). Each library was normalized
 individually according to the procedure described by
 Bonaldo, Lennon & Soares (genome Research 6:
 791-800, 1996). For construction of the DK0 subtracted
 library, plasmid DNA from each of the five individually
 tagged, normalized libraries was mixed in the proportions
 specified above and electroporated into competent bacteria
 for production of single-stranded circular DNA
 representing the pool of libraries. Single-stranded
 circular DNA representing these five normalized libraries
 was then used as a tracer in a subtractive hybridization
 with a driver (PCR amplified inserts from a plasmid DNA
 template preparation) comprising: a) a set of about 1,000
 arrayed clones from each of the five non-normalized
 libraries of brain (CROs), heart (CSOs), kidney (CUOs),
 aorta (CWOs), and placenta (CXOs). The resulting pool of
 approximately 5,000 clones represented about 33.3% of the
 final driver population. A set of about 2,000 arrayed
 clones from each of the five normalized libraries of brain
 (CTOs), heart (CSO), kidney (CUO), aorta (CWO), and
 placenta (CXO). The resulting pool of about 10,000 clones
 represented about 66.6% of the final driver population.
 TAG-LIB-UI-R-DK0
 TAG-TISSUE-rat heart pool
 TAG-SEQ-ATAAGATAC"

BASE COUNT 97 a 124 c 121 g 156 t 1 others
 ORIGIN
 Query Match 73.3%; Score 395; DB 13; Length 499;
 Best Local Similarity 88.0%; Pred. No. 7.6e-99;
 Matches 463; Conservative 0; Mismatches 11; Indels 52; Gaps 1;
 QY 6 AGAGACCTTTGGCGGCGCTAGCTGTGAGCGCTTCACTGTGTGTGACCAAGGG 65
 |||||
 Db 499 AGAGACCTTTGGCGGCGCTAGCTGTGAGCGCTTCACTGTGTGTGACCAAGGG 440
 QY 66 CTCTTACTTAACAGAGCCACAGCTCTATGGCTCAGATTGGAGGGACACAGCGGG 125
 |||||
 Db 439 CTCTTACTTAACAGAGCCACAGAGCTATGGCTCAGATTGGAGGGACACAGCGGG 380
 QY 126 CATTTGGATGAGTGTGCTTCCGAGCTGTGATCTGAGGAGGCTGAGATGTACTGTG 185
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 Db 379 CATTTGGATGAGTGTGCTTCCGAGCTGTGATCTGAGGAGGCTGAGATGTACTGTG 320
 QY 186 CCGCTGCAAGCTTACAGAGTACAGTCTGCTCCAGTCCGGGCCACGACACTACATGCC 245
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 Db 319 TCCGCTTAAGCTTACAGAGTACAGTCTGCTCCAGTCCGGGCCACGACACTACATGCC 260
 QY 246 CAAGACTCAGAGTCCAGCGCCCTATCGACACAGAAAGAAAGAGAGCTGCAAGGAGAG 305
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 Db 259 CAAGACTCAG----- 250
 QY 306 GAAGAGAGTACACTTGAAGACACAGAGTGAAGAGTGAAGAGAGAGAGACTACAGAA 365
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 Db 249 --AAGGAGAGTACACTTGAAGACACAGAGTGAAGAGTGAAGAGAGAGAGACTACAGAA 192
 QY 366 TGTAGAGAGAGCTCCCGAGAGACAGAAATGCCAGGTACCCGCAAGATCTTGTGCT 425
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 Db 191 TGTAGAGAGAGCTCCCGAGAGAGAGAAATGCCAGGTACCCGCAAGATCTTGTGCT 132
 QY 426 TGAGCAACCTGCAAAAGATGGAACACCTGCCAATATCATATATGAGTTCAATATCAT 485
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 Db 131 TGAGCAACCTGCAAAAGATGGAACACCTGCCAATATCATATATGAGTTCAATATCAT 72
 QY 486 TCAGAGATGGGCAATTTCCCTCAATGAATACAGAAAGTAACATTCC 531
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 Db 71 TCAGAGATGGGCAATTTCCCTCAATGAATACAGAAAGTAACATTCC 26

RESULT 15
LOCUS A1104669/c 502 bp mRNA linear EST 08-JAN-1999
DEFINITION RHCH40 3' end, mRNA sequence.
ACCESSION A1104669
VERSION A1104669.1 GI:4134279
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 502)
Lee, N.H., Glodet, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R., and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
Gene Index
Unpublished (1998)
On Oct 6, 1998 this sequence version replaced gi:3708981.
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1..502
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone_id="RHCH40"
/note="Normalized rat heart, Bento Soares"
/note="Organ: heart; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"

BASE COUNT 108 a 128 c 122 g 144 t
ORIGIN

Query Match 73.1%; Score 394.2; DB 9; Length 502;
Best Local Similarity 87.7%; Pred. No. 1.3e-98;
Matches 464; Conservative 0; Mismatches 13; Indels 52; Gaps 1;

QY 3 ACCAGAGACCCCTTGGGGGCTGAGCTGTGGAGCCTTTCAGTTGCTGTGACCAAG 62
DB 502 ACCAGAGACCCCTTGGGGGCTGAGCTGTGGAGCCTTTCAGTTGCTGTGACCAAG 443
QY 63 GGGCTTTACTTCAACAGCCACAGCTCTATGCTCCAGATTCGAGGGCACCACAGAC 122
DB 442 GGGCTTTACTTCAACAGCCACAGCTCTATGCTCCAGATTCGAGGGCACCACAGAC 383
QY 123 GGGCATTTGTGATGAGTGTGCTTCGGAGCTGTGATCTGAGGAGGCTGGAGTGTACTG 182
DB 382 GGGCATTTGTGATGAGTGTGCTTCGGAGCTGTGATCTGAGGAGGCTGGAGTGTACTG 323
QY 183 TGTCCGCTGCAAGCTACAAAGTCAGTGTGCTTCATCCGGCCAGCCACAGCTGACAT 242
DB 322 TGTCCGCTGCAAGCTACAAAGTCAGTGTGCTTCATCCGGCCAGCCACAGCTGACAT 263
QY 243 GCCCAAGACTCAGAAGTCCAGCCCTATCGACACAAAGAAAGAGAGCTGCAAGAGAG 302
DB 262 GCCCAAGACTCAG----- 250
QY 303 AAGGAAGGAAGTACACTTGAAGACAAAGTAGAGAGTAGAGAGTAGAGAGTAGAGAGTAGAG 362
DB 249 -----AAGGAAGTACACTTGAAGACAAAGTAGAGAGTAGAGAGTAGAGAGTAGAGAGTAGAG 195
QY 363 GAATGTAAGAGAGAGCTCCGAGAGAAAGAAATGCGACAGTCAACCGCAAGATCCTTGGCT 422
DB 194 GAATGTAAGAGAGAGCTCCGAGAGAAAGAAATGCGACAGTCAACCGCAAGATCCTTGGCT 135
QY 423 GCTTGAGCAACTGCAAAACATGGAACACCTGCCAAATATCAATATGAGTTCAATATC 482
DB 134 GCTTGAGCAACTGCAAAACATGGAACACCTGCCAAATATCAATATGAGTTCAATATC 75

DB 134 GCTTGAGCAACTGCAAAACATGGAACACCTGCCAAATATCAATATGAGTTCAATATC 75
QY 483 ATTTAGAGATGGGCAATTTCCCTCAATGAATACACAGTAACATTC 531
DB 74 ATTTAGAGATGGGCAATTTCCCTCAATGAATACACAGTAACATTC 26
Search completed: June 15, 2003, 18:18:23
Job time: 1148.61 secs